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USPT,JPAB,EPAB,DWPI,TDBD	norf	178	L2
USPT,JPAB,EPAB,DWPI,TDBD	(serial adj analysis) near5 (gene adj expression)	32	L3
USPT,JPAB,EPAB,DWPI,TDBD	nonannotated adj open adj reading adj frame	0	L4
USPT,JPAB,EPAB,DWPI,TDBD	non adj annotated adj open adj reading adj frame	0	L5
USPT,JPAB,EPAB,DWPI,TDBD	nonannotated adj orf	1	L6
USPT,JPAB,EPAB,DWPI,TDBD	non adj annotated adj orf	0	L7
USPT,JPAB,EPAB,DWPI,TDBD	gene$1 or dna$1 or cdna$1 or rna$1 or mrna$1	184925	L8
USPT,JPAB,EPAB,DWPI,TDBD	l1 or l2	6601	L9
USPT,JPAB,EPAB,DWPI,TDBD	l8 and l9	276	L10
USPT,JPAB,EPAB,DWPI,TDBD	435/6	11821	L11
USPT,JPAB,EPAB,DWPI,TDBD	l10 and l11	51	L12
USPT,JPAB,EPAB,DWPI,TDBD	l3 or l4 or l5 or l6 or l7	33	L13
USPT,JPAB,EPAB,DWPI,TDBD	l12 or l13	70	L14
USPT,JPAB,EPAB,DWPI,TDBD	l3 or l4 or l5 or l6 or l7	33	L15
USPT	l14	64	L16
USPT,JPAB,EPAB,DWPI,TDBD	l14 not l16	6	L17

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 1184 SAGE/AB
L1 2854 SAGE/BI,AB

=> s norf/bi/ab

 11 NORF/AB
 70716 BI/AB
L2 0 NORF/BI/AB
 ((NORF(W)BI)/AB)

=> s norf/bi,ab

 16 NORF/BI
 11 NORF/AB
L3 16 NORF/BI,AB

=> s (gene# or dna# or cdna# or rna# or mrna#)/bi,ab

 630469 GENE#/BI
 479589 GENE#/AB
 484945 DNA#/BI
 409922 DNA#/AB
 118507 CDNA#/BI
 101309 CDNA#/AB
 216393 RNA#/BI
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 168112 RNA#/AB
 178149 MRNA#/BI
 161163 MRNA#/AB
L4 1050532 (GENE# OR DNA# OR CDNA# OR RNA# OR
MRNA#)/BI,AB
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L1 2854 S SAGE/BI,AB
L2 0 S NORF/BI/AB
L3 16 S NORF/BI,AB
L4 1050532 S (GENE# OR DNA# OR CDNA# OR RNA# OR
MRNA#)/BI,AB
=> s l1 or l3

L5 2869 L1 OR L3

=> s l4 and l5

L6 167 L4 AND L5

=> s l6 not 2001/py

 8521 2001/PY
L7 167 L6 NOT 2001/PY

=> s l7 not 2000/py

 852055 2000/PY
L8 97 L7 NOT 2000/PY

=> s l8 not 1999/py

 899165 1999/PY
L9 50 L8 NOT 1999/PY

=> d l8 1-97 bib ab


L8 ANSWER 1 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:527842 CAPLUS
TI |Genes| differentially expressed in medulloblastoma
and fetal brain
AU Michiels, E. M. C.; Oussoren, E.; Van Groenigen,
M.; Pauws, E.; Bossuyt, P. M. M.; Voute, P. A.; Baas,
F.
CS Department of Pediatric Oncology, Emma
Kinderziekenhuis/Academic Medical Center, Amsterdam,
1100, Neth.
SO Physiol. Genomics (1999), 1, 83-91
 CODEN: PHGEFP; ISSN: 1094-8341
 URL:
http://physiolgenomics.physiology.org/cgi/reprint/1/2/
83.pdf PB American Physiological Society
DT Journal; (online computer file)
LA English
AB Serial anal. of |gene| expression ( |SAGE| ) was
used to identify |genes| that might be involved in the
development or growth of medulloblastoma, a childhood
brain tumor. Sequence tags from medulloblastoma
(10229) and fetal brain (10692) were detd. The
distributions of sequence tags in each population were
compared, and for each sequence tag, pairwise
.chi.-square test statistics were calcd. Northern blot
was used to confirm some of the results obtained by
|SAGE| . For 16 tags, the .chi.-square test statistic
was assocd. with a P value < 10-4. Among those
transcripts with a higher expression in
medulloblastoma were the |genes| for ZIC1 protein and
the OTX2 |gene| , both of which are expressed in the
cerebellar germinal layers. The high expression of
these two |genes| strongly supports the hypothesis
that medulloblastoma arises from the germinal layer of
the cerebellum. This anal. shows that |SAGE| can be
used as a rapid differential screening procedure.
RE.CNT 44
RE
(1) Adams, M; Science 1991, V252, P1651 CAPLUS
(3) Benedyk, M; Genes Dev 1994, V8, P105 CAPLUS
(7) Church, G; Proc Natl Acad Sci USA 1984, V81, P1991
CAPLUS (8) Cogen, P; Genomics 1990, V8, P279 CAPLUS
(10) Enoch, T; Mol Cell Biol 1986, V6, P801 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:143092 CAPLUS
DN 133:29723
TI Application of oxidative |DNA| damage measurements
to study antioxidant actions of dietary components
AU Aruoma, Okezie I.; Jenner, Andrew; Halliwell, Barry
CS Departamento de Analises Clinicas, Universidade de
Sao Paulo-Ribeirao Preto, Ribeirao Preto-Sao Paulo,
14040-903, Brazil
SO NATO ASI Ser., Ser. A (1999), 302(Advances in DNA
Damage and Repair), 19-26
 CODEN: NALSDJ; ISSN: 0258-1213
PB Kluwer Academic/Plenum Publishers
DT Journal; General Review
LA English
AB A review with 44 refs. Plant-derived antioxidants
such as flavonoids, vitamin E, vitamin C,
.beta.-carotene or rosemary and |sage| exts. are
increasingly proposed as important dietary antioxidant
factors. In this article, assays for characterizing
the potential prooxidant and antioxidant actions of
food additives, antioxidant supplements, antioxidant
drug mols. and nutrient components based on the
assessment of products of |DNA| oxidn. are reviewed.
RE.CNT 44
RE
(1) Anton, R; Plant Flavonoids in Biology and Medicine
II: Biochemical and Medicinal Properties 1988, P423
CAPLUS
(5) Aruoma, O; Fd Chem Toxicol 1994, V32, P671 CAPLUS
(7) Aruoma, O; Free Rad Res Commun 1990, V10, P143
CAPLUS
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(8) Aruoma, O; Meth Enzymol 1994, V233, P57 CAPLUS
(10) Aruoma, O; Xenobiotica 1992, V22, P257 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:103580 CAPLUS
DN 133:115561
TI Serial analysis of |gene| expression: probing transcriptomes for molecular targets
AU Lal, Anita; Siu, I-Mei; Riggins, Gregory J.
CS Department of Pathology, Duke University Medical Center, Durham, NC, 27710, USA
SO Curr. Opin. Mol. Ther. (1999), 1(6), 720-726
CODEN: CUOTFO; ISSN: 1464-8431
PB Current Drugs Ltd.
DT Journal; General Review
LA English
AB A review with 39 refs. Serial anal. of |gene| expression (|SAGE|) is a method to rapidly count expressed |RNA| transcripts in a population of cells. The basic approach is to isolate a small transcript tag, clone multiple tags into a sequencing vector and efficiently count the tags by automated sequencing. The result is the fractional representation of nearly every transcript (the transcriptome), in a digital format. These tag counts can be compared to other |SAGE| libraries yielding differentially expressed |genes| . Anal. of the differentially expressed |genes| has been used to det. which |genes| are involved in a disease process. The promise of this technol. is that by understanding when |genes| are pathol. altered in expression, therapies can be formulated to target the appropriate |gene| or pathway.
RE.CNT 38
RE
(2) Basrai, M; Mol Cell Biol 1999, V19, P7041 CAPLUS
(3) Bunz, F; Science 1998, V282, P1497 CAPLUS
(5) Datson, N; Nucleic Acids Res 1999, V27, P1300 CAPLUS
(6) de Waard, V; Gene 1999, V226, P1 CAPLUS
(7) Facchinetti, F; Cell Mol Neurobiol 1998, V18, P667
CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:99785 CAPLUS
DN 132:247039
TI Transcript profiling in rice (Oryza sativa L.) seedlings using serial analysis of |gene| expression (|SAGE|) AU Matsumura, Hideo; Nirasawa, Shizuko; Terauchi, Ryohei CS Iwate Biotechnology Research Center, Narita, 024-0003, Japan SO Plant J. (1999), 20(6), 719-726
CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB Serial anal. of |gene| expression (|SAGE|) was applied for profiling expressed |genes| in rice seedlings. In the |SAGE| method, a 9-11 bp fragment (tag) represents each transcript, and frequency of a tag in the sample directly reflects the abundance of the resp. |mRNA| . The authors studied 10,122 tags derived from 5921 expressed |genes| in rice (Oryza sativa) seedings, among which only 1367 |genes| (23.1%) matched the rice |cDNA| or EST sequences in the |DNA| database. |SAGE| showed that most of the highly expressed |genes| in rice seedlings belong to the category of housekeeping |genes| (|genes| encoding ribosomal proteins or proteins responsible for metab. and cell structure). Unexpectedly, the most highly expressed |gene| in rice seedlings was a metallothionein (MT) |gene| , and together with 3 other messages for MT, it accounts for 2.7% of total |gene| expression. To our knowledge, this is the first quant. study of global |gene| expression in a higher plant. Further, the |SAGE| technique was applied to identify differentially expressed |genes| between anaerobically treated and untreated rice seedlings. Addnl., a longer |cDNA| fragment can be easily recovered by PCR using the |SAGE| tag sequence as a primer, thereby facilitating the anal. of unknown |genes| identified by tag sequence in |SAGE| . In combination with microarray anal., |SAGE| should serve as a highly efficient tool for the identification and isolation of differentially expressed |genes| in plants.
RE.CNT 29
RE
(2) Cho, H; Plant Cell 1997, V9, P1661 CAPLUS
(3) Claes, B; Plant Cell 1990, V2, P19 CAPLUS
(4) Cooke, R; Plant J 1996, V9, P101 CAPLUS
(5) Datson, N; Nucl Acids Res 1999, V27, P1300 CAPLUS
(6) DeWald, D; J Biol Chem 1992, V267, P15958 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 5 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:55686 CAPLUS
DN 132:191665
TI Antibacterial activities of cryptotanshinone and dihydrotanshinone I from a medicinal herb, Salvia miltiorrhiza bunge
AU Lee, Dong-Sun; Lee, Sang-Han; Noh, Jae-Geun; Hong, Soon-Duck CS Department of Microbiology, College of Natural Science, Kyungpook National University, Taegu, 702-701, S. Korea
SO Biosci., Biotechnol., Biochem. (1999), 63(12), 2236-2239 CODEN: BBBIEJ; ISSN: 0916-8451
PB Japan Society for Bioscience, Biotechnology, and Agrochemistry DT Journal
LA English
AB Cryptotanshinone (I) and dihydrotanshinone I (II), constituents of a medicinal plant, Salvia miltiorrhiza Bunge, had antibacterial activity against a broad range of Gram pos. bacteria. These compds. generated superoxide radicals in Bacillus subtilis lysates. A recombination- deficient mutant strain of B. subtilis was 2- to 8-fold more sensitive than a wild strain, and this hypersensitivity was reduced in the presence of dithiothreitol as an antioxidant. |DNA| , |RNA| ,

and protein syntheses in B. subtilis were non-selectively inhibited by these compds. These results suggest that superoxide radicals are important in the antibacterial actions of the agents. antibacterial activity. RE.CNT 11
RE
(1) Lee, A; J Nat Prod 1987, V50, P157 CAPLUS
(2) Lee, D; Biosci Biotechnol Biochem 1999, V63, P1370 CAPLUS (3) Lee, D; J Microbiol Biotechnol 1998, V8, P89 CAPLUS
(5) Love, P; Proc Natl Acad Sci USA 1985, V82, P6201 CAPLUS (6) Michelson, A; Agents Actions Suppl 1982, V11, P179 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:47162 CAPLUS
DN 132:216680
TI Tanshinone IIA, an ingredient of Salvia miltiorrhiza BUNGE, induces apoptosis in human leukemia cell lines through the activation of caspase-3 AU Sung, Hyun Jea; Choi, Sun Mi; Yoon, Yoosik; An, Kyu Suk CS Korea Institute of Oriental Medicine, Seoul, 135-100, S. Korea SO Exp. Mol. Med. (1999), 31(4), 174-178
CODEN: EMMEF3; ISSN: 1226-3613
PB Korean Society of Medical Biochemistry and Molecular Biology DT Journal
LA English
AB Tanshinone II-A is a deriv. of phenanthrene-quinone isolated from Salvia miltiorrhiza BUNGE, a traditional herbal medicine that is known to induce antiinflammatory, anti-oxidative and cytotoxic activity. We have examd. cellular effects of Tanshione II-A on HL60 human promyelocytic leukemic cells and K562 human erythroleukemic cells. Tanshione II-A induced a dose- and time-dependent |DNA| fragmentation into the multiples of 180 bp and specific proteolytic cleavage of poly(ADP-ribose) polymerase in both cell lines. PI-staining and flow cytometry anal. of K562 cells following Tanshione II-A treatment showed an increase of the cells possessing hypodiploid |DNA| indicative of apoptotic state of cells. Caspase-3 activity was significantly increased during Tanshinone II-A treatment of both HL60 and K562 cells, whereas caspase-1 activity was not changed. These results suggest that Tanshione II-A induced HL60 and K562 cellular apoptosis that may be assocd. with the selective members of caspase family.
RE.CNT 13
RE
(2) Cohen, G; Biochem J 1992, V286, P331 CAPLUS
(4) Kamesaki, H; Int J Hematol 1998, V68, P29 CAPLUS
(5) Martins, L; Blood 1997, V90, P4283 CAPLUS
(6) Nicholson, D; Nature 1995, V376, P37 CAPLUS
(7) Ryu, S; Planta Med 1997, V63, P339 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 7 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:30840 CAPLUS
DN 132:332628
TI Molecular pathology and future developments
AU Going, J. J.; Gusterson, B. A.
CS Dep. Pathol., Glasgow Royal Infirmary, Univ. Glasgow, Glasgow, G4 0SF, UK SO Eur. J. Cancer (1999), 35(14), 1895-1904
CODEN: EJCAEL; ISSN: 0959-8049
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review, with 76 refs. There has already been a 'mol.' revolution in pathol. Demonstrating transcription of specific single |genes| or small |gene| sets and translation of their protein products by in situ hybridization and immunocytochem. is routine in diagnostic and exptl. pathol. A perhaps-greater revolution is imminent with the application of more recently established and emergent technologies in pathol. These include new approaches to polymerase chain reaction (PCR); simultaneous studies of multiple |genes| and their expression using oligonucleotide and |cDNA| arrays; serial anal. of |gene| expression (|SAGE|); expressed sequence tag (EST) sequencing, subtractive cloning, and differential display; high-throughput sequencing; comparative genomic hybridization and multiplex fluorescence in situ hybridization (FISH) (spectral karyotyping); reverse chromosome painting; knockout and transgenic organisms; laser microdissection and micromachining; and new methods in bioinformatics, 'data mining', and data visualization. Mol. methods will profoundly change diagnosis, prognosis, and treatment targeting in oncol. and elucidate fundamental mechanisms of neoplastic transformation. Individual susceptibility to specific diseases will become assessable, and screening will be refined. The new mol. biol. will be most fruitful in partnership with classical approaches to pathol.: the expectation that mol. methods alone will answer all pathol. questions is unrealistic. A further challenge for the biomedical community in the 'genome era' will be to ensure that the benefits of these sophisticated technologies are enjoyed globally.
RE.CNT 77
RE
(1) Arkesteijn, G; Cytometry 1999, V35, P117 CAPLUS
(3) Banks, R; Electrophoresis 1999, V20, P689 CAPLUS
(6) Bertelsen, A; Drug Discovery Today 1998, V3, P152 CAPLUS (11) Bubendorf, L; Cancer Res 1999, V59, P803 CAPLUS
(12) Cardiff, R; Adv Oncobiol 1998, V2, P177 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 8 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:11317 CAPLUS
DN 132:232473
TI Serial microanalysis of renal transcriptomes
AU Virlon, Berangere; Cheval, Lydie; Buhler, Jean-Marie; Billon, Emmanuelle; Doucet, Alain; Elalouf, Jean-Marc

CS Departement de Biologie Cellulaire et Moleculaire, Service de Biologie Cellulaire, Centre National de la Recherche Scientifique Unite de Recherche Associee 1859, Gif-sur-Yvette, 91191, Fr.
SO Proc. Natl. Acad. Sci. U. S. A. (1999), 96(26), 15286-15291 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Large-scale |gene| expression studies can now be routinely performed on macroamounts of cells, but it is unclear to which extent current methods are valuable for analyzing complex tissues. In the present study, serial anal. of |gene| expression (|SAGE|) was used for quant. |mRNA| profiling in the mouse kidney. |SAGE| was first performed at the whole-kidney level by sequencing 12,000 |mRNA| tags. Most abundant tags corresponded to transcripts widely distributed or enriched in the predominant kidney epithelial cells (proximal tubular cells), whereas transcripts specific for minor cell types were barely evidenced. To better explore such cells, a |SAGE| adaptation for downsized exts. was developed, enabling a 1000-fold redn. of the amt. of starting material. The potential of this approach was evaluated by studying |gene| expression in microdissected kidney tubules (50,000 cells). Specific |gene| expression profiles were obtained, and known markers (e.g., uromodulin in the thick ascending limb of Henle's loop and aquaporin-2 in the collecting duct) were found appropriately enriched. In addn., several enriched tags had no databank match, suggesting that they correspond to unknown or poorly characterized transcripts with specific tissue distribution. It is concluded that |SAGE| adaptation for downsized exts. makes possible large-scale quant. |gene| expression measurements in small biol. samples and will help to study the tissue expression and function of |genes| not evidenced with other high-throughput methods.
RE.CNT 21
RE
(2) Chabardes, D; J Biol Chem 1996, V271, P19264 CAPLUS
(3) Chomczynski, P; Anal Biochem 1987, V162, P156 CAPLUS
(4) Datson, N; Nucleic Acids Res 1999, V27, P1300 CAPLUS
(5) DeRisi, J; Science 1997, V278, P680 CAPLUS
(6) Gress, T; Mamm Genome 1992, V3, P609 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 9 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 2000:4655 CAPLUS
DN 132:118210
TI Male-driven evolution among ecaves? A test of the replicative division hypothesis in a heterogametic female (ZW) system
AU Kahn, Nate W.; Quinn, Tom W.
CS Department of Biological Sciences, University of Denver, Denver, CO, 80208, USA
SO J. Mol. Evol. (1999), 49(6), 750-759
CODEN: JMEVAU; ISSN: 0022-2844
PB Springer-Verlag New York Inc.
DT Journal
LA English
AB Because avian females are heterogametic, the reverse of mammals, avian sex chromosomes undergo significantly different patterns and nos. of |DNA| replications than do those in mammals. This makes the W (female-specific) and the Z chromosomes an excellent model system for the study of the replicative division hypothesis, which purports that |DNA| substitution rate is detd. by the no. of germline replications. The sex-specific chromosome in birds (the W) is predicted to change at the slowest rate of all avian chromosomes because it undergoes the fewest rounds of replication per unit of evolutionary time. Using published data on gametogenesis from a variety of sources, we estd. the ratio of male-to-female germline replications (c) in galliforms and anseriforms to be approx. 4.4. The value of c should predict the value of the ratio of male-to-female mutation rates (.alpha.m) if the replicative division hypothesis is true. Homologous |DNA| sequences including an intron and parts of two exons of the CHD |gene| were obtained from the W and the Z chromosomes in ostrich, |sage| grouse, canvasback duck, tundra swan, and snow goose. The exons show significantly different nucleotide compn. from the introns, and the W-linked exons show evidence of relaxed constraint. The Z-linked intron is diverging .apprxeq. 3.1 times faster than the W-linked intron. From this, .alpha.m was calcd. to be approx. 4.1, with a confidence interval of 3.1 to 5.1. The data support the idea that the no. of replicative divisions is a major determinant of substitution rate in the Eoavian genome.
RE.CNT 89
RE
(1) Alvarez-Valin, F; J Mol Evol 1998, V46, P37 CAPLUS
(3) Bernardi, G; J Mol Evol 1993, V37, P583 CAPLUS
(4) Britten, R; Science 1986, V231, P1393 CAPLUS
(5) Brown, W; J Mol Evol 1982, V18, P225 CAPLUS
(6) Caccio, S; J Mol Evol 1995, V40, P280 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 10 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:783901 CAPLUS
DN 132:26672
TI Antiaging cosmetic composition containing a salt or a divalent metal complex
IN Bonte, Frederic; Dumas, Marc; Heusele, Catherine; Le Blay, Jacques PA Guerlain S.A., Fr.; Le Blay, Jacques
SO PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DT Patent
LA French
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9962481 A1 19991209 WO 1999-FR1261 19990528 W: JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
FR 2779059 A1 19991203 FR 1998-6822 19980529 PRAI FR 1998-6822 19980529
US 1999-297679 19990506
AB A cosmetic treatment method for fighting against skin ageing effects is disclosed. The invention is characterized in that it consists in using at least one agent promoting the adherence of basal layer keratinocytes to the dermal-epidermal junction, particularly to said junction's collagen IV such as in particular a salt or a divalent metal complex, preferably magnesium aspartate or magnesium chloride optionally assocd. with an agent stimulating collage IV synthesis and/or an agent stimulating collagen VII synthesis. The invention is useful for prepg. cosmetic compns. with anti-wrinkle activity. Efficacy of 1 mM magnesium chloride and 0.25 mM magnesium aspartate in promotion of adherence of human keratinocytes to the collagen type IV is shown. An antiwrinkle cram contained magnesium L-aspartate 0.3, Potentilla erecta 0.01, sodium hyaluronate 0.06, glycerol 5.15, Centella asiatica 0.1, vitamin A palmitate 0.1, vitamin E acetate 0.5, Perilla dry ext. 0.5, excipients, fragrances, and preservatives q.s. 100 g.
RE.CNT 10
RE
(1) Boiron, S; FR 2704390 A 1994 CAPLUS
(2) LVMH Recherche; FR 2669225 A 1992 CAPLUS
(3) LVMH Recherche; FR 2735981 A 1997 CAPLUS
(5) Lvmh Recherche; WO 9819664 A 1998 CAPLUS
(6) Messac, L; FR 2406438 A 1979 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 11 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:776080 CAPLUS
DN 132:19261
TI Differential |gene| expression
AU Eickhoff, Bodo
CS Kiel, Germany
SO BioTec (Marktheidenfeld, Ger.) (1999), 10(5), 58-59,62,67 CODEN: BWGEE9; ISSN: 0937-2725
PB MediaTec Verlag und -Service
DT Journal; General Review
LA German
AB A brief review with 4 refs. and 5 internet addresses is given on methods of differential |gene| expression. Differential, complex, and substractive hybridization as well as differential display reverse transcriptase PCR and serial anal. of |gene| expression (|SAGE|) are described. Advantages and expense are compared.

L8 ANSWER 12 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:764996 CAPLUS
DN 132:220267
TI Identification of changes in |gene| expression associated with minimal residual disease
AU Kao, Ruey Ho; Von Schlippe, Maria; Francia, Giulio; Powell, Jill; Hart, Ian R.
CS Richard Dimbleby Department of Cancer Research/Imperial Cancer Research Fund, Rayne Institute, St. Thomas' Hospital, London, UK SO Cancer Metastasis Rev. (1999), 18(1), 3-13
CODEN: CMRED4; ISSN: 0167-7659
PB Kluwer Academic Publishers
DT Journal; General Review
LA English
AB A review, with 56 refs. Minimal residual disease (MRD), the tumor burden which remains after a course of treatment that has resulted in clin. remission, appears to differ in certain characteristics from the primary tumor population. Certainly the cells which comprise MRD have had to escape from the constraints of the primary tumor mass, invade normal tissue and penetrate small vessels in order to enter the circulation in which they then have had to survive. Such activities are the consequence of the expression of specific proteins and these may well be a reflection of alterations in |DNA| or |RNA| levels. Identifying the changes in |RNA| expression levels between related cell groups exhibiting different phenotypes recently has become a great deal easier as a consequence of developments in anal. procedures such as Differential Display (DD) and Serial Anal. of |Gene| Expression (|SAGE|). Application of these procedures to MRD cells recovered from blood, bone marrow or lymph node, should identify novel sequences assocd. with tumor progression and the development of disseminated disease. RE.CNT 56
RE
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(2) Barraclough, R; Eur J Cancer 1994, V30A, P1570 CAPLUS
(7) Davies, B; Cancer Res 1994, V54, P2785 CAPLUS
(8) DeRisi, J; Nat Genet 1996, V14, P457 CAPLUS
(9) Diatchenko, L; Proc Natl Acad Sci 1996, V93, P6025 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 13 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:761983 CAPLUS
TI Tantalizing transcriptomes- |SAGE| and its use in global |gene| expression analysis
AU Velculescu, Victor E.
CS Johns Hopkins Oncology Center, Baltimore, MD, 21231, USA SO Science (Washington, D. C.) (1999), 286(5444), 1491-1492 CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English
AB Unavailable
RE.CNT 16
RE
(1) Adams, M; Nature 1995, V377, P3 CAPLUS
(2) Basrai, M; Mol Cell Biol 1999, V19, P7041 CAPLUS
(3) Goffeau, A; Science 1996, V274, P546 CAPLUS
(4) He, T; Science 1998, V281, P1509 CAPLUS
(7) Hibi, K; Cancer Res 1998, V58, P5690 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 14 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:746631 CAPLUS
DN 132:92199
TI Serial analysis of |gene| expression in HIV-1-infected T cell lines
AU Ryo, A.; Suzuki, Y.; Ichiyama, K.; Wakatsuki, T.; Kondoh, N.; Hada, A.; Yamamoto, M.; Yamamoto, N.
CS School of Medicine, Departments of Microbiology and Molecular Virology, Tokyo Medical and Dental University, Tokyo, Japan
SO FEBS Lett. (1999), 462(1,2), 182-186
CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB The |gene| expression profile of the HIV-1 infection state was analyzed in the human T cell line MOLT-4. Using the serial anal. of |gene| expression (|SAGE|) method, a total of 142{ omitted}603 |SAGE| tags were sequenced and identified, representing 43{ omitted}581 unique |mRNA| species. Comparison of expression patterns revealed that 53 cellular |genes| were differentially expressed upon HIV-1 infection. Northern blot and RT-PCR analyses confirmed the altered expression of the |genes| in both MOLT-4 and MT-4 cells. Up-regulated |genes| were mainly composed of transcription factors and |genes| related to T cell activation, whereas down-regulated |genes| were comprised of mitochondrial proteins, actin-related factors and translational factors. These findings indicate that persistent T cell activation, which may accelerate HIV-1 replication, and the disruption of cellular housekeeping |genes| including those involved in anti-apoptotic systems, may play an important role in HIV-1-induced pathogenesis.
RE.CNT 30
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 15 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:733425 CAPLUS
DN 132:88288
TI From the molecular biology of prolactin and its receptor to the lessons learned from knockout mice models
AU Goffin, V.; Binart, N.; Clement-Lacroix, P.; Bouchard, B.; Bole-Feysot, C.; Edery, M.; Lucas, B. K.; Touraine, P.; Pezet, A.; Maaskant, R.; Pichard, C.; Helloco, C.; Baran, N.; Favre, H.; Bernichtein, S.; Allamando, A.; Ormandy, C.; Kelly, P. A.
CS Faculte de Medecine Necker, INSERM Unite 344-Endocrinologie Moleculaire, Paris, 75730, Fr.
SO Genet. Anal.: Biomol. Eng. (1999), 15(3-5), 189-201
CODEN: GEANF4; ISSN: 1050-3862
PB Elsevier Science B.V.
DT Journal; General Review
LA English
AB A review, with 98 refs. Prolactin (PRL), a polypeptide hormone secreted mainly by the pituitary and, to a lesser extent, by peripheral tissues, affects more physiol. processes than all other pituitary hormones combined since it is involved in > 300 sep. functions in vertebrates. Its main actions are related to lactation and reprodn. The initial step of PRL action is the binding to a specific membrane receptor, the PRLR, which belongs to the class 1 cytokine receptor superfamily. PRL-binding sites have been identified in a no. of tissues and cell types in adult animals. Signal transduction by this receptor is mediated, at least in part, by two families of signaling mols.: Janus tyrosine kinases and signal transducers and activators of transcription (STATs). Disruption of the PRLR |gene| has provided a new mouse model with which to identify actions directly assocd. with PRL or any other PRLR ligands, such as placental lactogens. To date, several different phenotypes have been analyzed and are briefly described in this review. Coupled with the |SAGE| technique, this PRLR knockout model is being used to qual. and quant. evaluate the expression pattern of hepatic |genes| in two physiol. situations: transcriptomes corresponding to livers from both wild type and PRLR KO mice are being compared, and following statistical analyses, candidate |genes| presenting a differential profile will be further characterized. Such a new approach will undoubtedly open future avenues of research for PRL targets. To date, no pathol. linked to any mutation in the |genes| encoding PRL or its receptor have been identified. The development of genetic models provides new opportunities to understand how PRL can participate to the development of pathologies throughout life, as for example the initiation and progression of breast cancer.
RE.CNT 98
RE
(1) Adams, T; J Biol Chem 1998, V273, P1285 CAPLUS
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(4) Arden, K; Cytogenet Cell Genet 1990, V53, P161 CAPLUS
(6) Bataille-Simoneau, N; Biochem Biophys Res Commun 1996, V229, P323 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 16 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:732780 CAPLUS
DN 132:91024
TI A population genetic comparison of large- and small-bodied |sage| grouse in Colorado using microsatellite and mitochondrial |DNA| markers

AU Oyler-McCance, S. J.; Kahn, N. W.; Burnham, K. P.; Braun, C. E.; Quinn, T. W.
CS Department of Fishery and Wildlife Biology, Colorado State University, Fort Collins, CO, 80523, USA
SO Mol. Ecol. (1999), 8(9), 1457-1465
CODEN: MOECEO; ISSN: 0962-1083
PB Blackwell Science Ltd.
DT Journal
LA English
AB |Sage| grouse (Centrocercus urophasianus) from southwestern Colorado and southeastern Utah (United States) are 33% smaller than all other |sage| grouse and have obvious plumage and behavioral differences. Because of these differences, they have been tentatively recognized as a sep. small-bodied species. We collected genetic evidence to further test this proposal, using mitochondrial sequence data and microsatellite markers to det. whether there was |gene| flow between the 2 proposed species. Significant differences in the distribution of alleles between the large- and small-bodied birds were found in both data sets. Anal. of mol. variance (AMOVA) revealed that 65% of the variation in mitochondrial |DNA| (mtDNA) haplotypes could be explained by the large- vs. small-bodied distinction. Genetic distances and neighbor-joining trees based on allelic frequency data showed a distinct sepn. between the proposed species, although cladistic anal. of the phylogenetic history of the mitochondrial sequence haplotypes has shown a lack of reciprocal monophyly. These results further support the recognition of the small-bodied |sage| grouse as a distinct species based on the biol. species concept, providing addnl. genetic evidence to augment the morphol. and behavioral data. Furthermore, small-bodied |sage| grouse had much less genetic variation than large-bodied |sage| grouse, which may have implications for conservation issues.
RE.CNT 31
RE
(9) Cheng, H; Poultry Science 1995, V74, P1855 CAPLUS
(11) Excoffier, L; Genetics 1992, V131, P479 CAPLUS
(21) Piertney, S; Molecular Ecology 1997, V6, P93 CAPLUS
(22) Quinn, T; Molecular Biology and Evolution 1987, V4, P126 CAPLUS (23) Quinn, T; Molecular Ecology 1992, V1, P105 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 17 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:725089 CAPLUS
DN 132:74143
TI Combining serial analysis of |gene| expression and array technologies to identify |genes| differentially expressed in breast cancer
AU Nacht, Mariana; Ferguson, Anne T.; Zhang, Wen; Petroziello, Joseph M.; Cook, Brian P.; Gao, Yu Hong; Maguire, Sharon; Riley, Deborah; Coppola, George; Landes, Gregory M.; Madden, Stephen L.; Sukumar, Saraswati CS Genzyme Molecular Oncology, Framingham, MA, 01701, USA SO Cancer Res. (1999), 59(21), 5464-5470
CODEN: CNREA8; ISSN: 0008-5472
PB AACR Subscription Office
DT Journal
LA English
AB Several methods have been used recently to det. |gene| expression profiles of cell populations. Here we demonstrate the strength of combining two approaches, serial anal. of |gene| expression (|SAGE|) and |DNA| arrays, to help elucidate pathways in breast cancer progression by finding |genes| consistently expressed at different levels in primary breast cancers, metastatic breast cancers, and normal mammary epithelial cells. |SAGE| profiles of 21PT and 21MT, two well-characterized breast tumor cell lines, were compared with |SAGE| profiles of normal breast epithelial cells to identify differentially expressed |genes| . A subset of these candidates was then placed on an array and screened with clin. breast tumor samples to find |genes| and expressed sequence tags that are consistently expressed at different levels in diseased and normal tissues. In addn. to finding the predicted overexpression of known breast cancer markers HER-2/neu and MUC-1, the powerful coupling of |SAGE| and |DNA| arrays resulted in the identification of |genes| and potential pathways not implicated previously in breast cancer. Moreover, these techniques also generated information about the differences and similarities of expression profiles in primary and metastatic breast tumors. Thus, combining |SAGE| and custom array technol. allowed for the rapid identification and validation of the clin. relevance of many |genes| potentially involved in breast cancer progression. These differentially expressed |genes| may be useful as tumor markers and prognostic indicators and may be suitable targets for various forms of therapeutic intervention.
RE.CNT 49
RE
(2) Bachem, C; Plant J 1996, V9, P745 CAPLUS
(3) Band, V; Cancer Res 1990, V50, P7351 CAPLUS
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(8) Chandrasekharappa, S; Science 1997, V276, P404 CAPLUS
(9) Chiappetta, G; Oncogene 1995, V10(7), P1307 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 18 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:725074 CAPLUS
DN 132:49567
TI A public database for |gene| expression in human cancers AU Lal, Anita; Lash, Alex E.; Altschul, Stephen F.; Velculescu, Victor; Zhang, Lin; McLendon, Roger E.; Marra, Marco A.; Prange, Christa; Morin, Patrice J.; Polyak, Kornelia; Papadopoulos, Nickolas; Vogelstein, Bert; Kinzler, Kenneth W.; Strausberg, Robert L.; Riggins, Gregory J. CS Department of Pathology, Duke University Medical Center, Durham, NC, 27710, USA

SO Cancer Res. (1999), 59(21), 5403-5407
CODEN: CNREA8; ISSN: 0008-5472
PB AACR Subscription Office
DT Journal
LA English
AB A public database, SAGEmap, was created as a component of the Cancer Genome Anatomy Project to provide a central location for depositing, retrieving, and analyzing human |gene| expression data. This database uses serial anal. of |gene| expression to quantify transcript levels in both malignant and normal human tissues. By accessing SAGEmap (http://www.ncbi.nlm.nih-gov/ |SAGE|) the user can compare transcript populations between any of the posted libraries. As an initial demonstration of the database's utility, |gene| expression in human glioblastomas was compared with that of normal brain white matter. Of the 47, 174 unique transcripts expressed in these two tissues, 471 were differentially expressed by more than 5-fold (P < 0.001). Classification of these |genes| revealed functions consistent with the biol. properties of glioblastomas, in particular: angiogenesis, transcription, and cell cycle related |genes| . RE.CNT 20
RE
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(2) Gilboa, E; Cancer Immunol Immunother 1998, V46, P82 CAPLUS (3) He, T; Science (Washington DC) 1998, V281, P1509 CAPLUS (4) Hermeking, H; Mol Cell 1997, V1, P3 CAPLUS
(5) Hibi, K; Cancer Res 1998, V58, P5690 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 19 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:688232 CAPLUS
DN 132:260259
TI Tanshinone IIA isolated from Salvia miltiorrhiza Bunge induced apoptosis in HL60 human premyelocytic leukemia cell line
AU Yoon, Y.; Kim, Y.-O.; Jeon, W.-K.; Park, H.-J.; Sung, H. J. CS Laboratory of Cancer Research, Korea Institute of Oriental Medicine, Seoul, S. Korea
SO J. Ethnopharmacol. (1999), 68(1-3), 121-127
CODEN: JOETD7; ISSN: 0378-8741
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Tanshinone IIA was isolated from S. miltiorrhiza, a traditional oriental medical herb; it induced apoptosis in the HL60 human premyelocytic leukemia cell line. Tanshinone IIA induced |DNA| fragmentation into multiples of 180 bp and increased the percentage of hypodiploid cells as shown by flow cytometry after propidium iodide staining. Tanshinone IIA-induced apoptosis was accompanied by the specific proteolytic cleavage of poly(ADP-ribose) polymerase and the activation of caspase-3, a major component in the mechanism of apoptotic cell death.
RE.CNT 14
RE
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(6) Onitsuka, M; Chemical Pharmaceutical Bulletin 1983, V31, P1670 CAPLUS (7) Park, H; Journal of Korean Society of Food and Nutrition 1995, V24, P459 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 20 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:644863 CAPLUS
DN 132:164271
TI PGP9.5 as a candidate tumor marker for non-small-cell lung cancer AU Hibi, Kenji; Westra, William H.; Borges, Michael; Goodman, Steve; Sidransky, David; Jen, Jin
CS Department of Otolaryngology-Head and Neck Surgery, Division of Head and Neck Cancer Research, Johns Hopkins University School of Medicine, Baltimore, MD, 21205-2196, USA
SO Am. J. Pathol. (1999), 155(3), 711-715
CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal
LA English
AB PGP9.5 is a neurospecific peptide that functions to remove ubiquitin from ubiquitinated proteins and prevents them from targeted degrdn. by proteasomes. Using the serial anal. of |gene| expression method (|SAGE|), the authors obsd. that the PGP9.5 transcript was highly expressed in primary lung cancers and lung cancer cell lines but was not detectable in the normal lung. Here, the authors examd. the expression of PGP9.5 protein in normal lung epithelium, lung tumor cell lines, and 98 resected primary non-small-cell lung carcinomas (NSCLCs). The authors found PGP9.5 reactivity in normal lung in a pattern compatible with K-cells of the diffuse neuroendocrine system. However, the PGP9.5 was present in both small-cell lung cancer (SCLC) and NSCLC cell lines (22/24) independent of neuronal differentiation. In primary NSCLCs, 54% (53/98) of the cases had pos. PGP9.5 staining, and the expression of protein was strongly assocd. with pathol. stage of the cancer. It was present in 44% (29/66) of stage I NSCLCs and in 75% (24/32) of stage II and IIIA NSCLCs. These results suggest that the increased expression of PGP9.5 is specifically assocd. with lung cancer development and may serve as a potential marker for the detection of lung cancer.
RE.CNT 26
RE
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(4) Borges, M; Nature 1997, V386, P852 CAPLUS
(5) Day, I; FEBS Lett 1987, V210, P157 CAPLUS
(7) Diehl, J; Genes Dev 1997, V11, P957 CAPLUS
(8) Gray, D; Oncogene 1995, V10, P2179 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 21 OF 97 CAPLUS COPYRIGHT 2001 ACS

AN 1999:640866 CAPLUS
DN 131:267938
TI Oligonucleotides and methods for identification of lung tumor cells IN Beaudry, Gary A.; Madden, Stephen L.; Bertelsen, Arthur H. PA Genzyme Corp., USA
SO PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9950278	A1	19991007	WO 1999-US6938	19990330
AU 9932168	A1	19991018	AU 1999-32168	19990330

PI WO 9950278 A1 19991007 WO 1999-US6938 19990330 W: AU, CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AU 9932168 A1 19991018 AU 1999-32168 19990330 PRAI US 1998-80037 19980331
AB This invention provides compns. and methods for the identification of lung cancer cells. In particular, polynucleotide sequences whose presence is indicative of lung cancer are disclosed. In addn., lung cancer can be identified by detecting the presence of the peptides encoded by these sequences. Antibodies to these peptides are also provided. Also included are |gene| delivery vehicles and host cells comprising these polynucleotides. Kits contg. agents and instructions necessary to perform the screening and detecting methods are also provided. Thus, a systematic anal. of transcripts present in non-small cell lung cancer was performed by |SAGE| (serial anal. of |gene| expression). 40 Oligonucleotide tags were generated which corresponded to 20 known |genes| as well as 20 unknown |genes| , half of correspond to previously reported ESTs.
RE.CNT 5
RE
(1) Biogen Inc; WO 89/09818 A1 1989 CAPLUS
(2) Dryja; WO 89/06703 A1 1989 CAPLUS
(3) McGuire; US 5447843 A 1995 CAPLUS
(4) Srivastava; US 5830464 A 1998 CAPLUS
(5) The General Hospital Corporation; WO 90/05745 A1 1990 CAPLUS

L8 ANSWER 22 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:632622 CAPLUS
DN 131:334530
TI NORF5/HUG1 is a component of the MEC1-mediated checkpoint response to |DNA| damage and replication arrest in Saccharomyces cerevisiae AU Basrai, Munira A.; Velculescu, Victor E.; Kinzler, Kenneth W.; Hieter, Philip
CS Department of Molecular Biology & Genetics, The Johns Hopkins University School of Medicine, Baltimore, MD, 21205, USA
SO Mol. Cell. Biol. (1999), 19(10), 7041-7049
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Anal. of global |gene| expression in Saccharomyces cerevisiae by the serial anal. of |gene| expression technique has permitted the identification of at least 302 previously unidentified transcripts from nonannotated open reading frames (NORFs). Transcription of one of these, NORF5/HUG1 (hydroxyurea and UV and gamma radiation induced), is induced by |DNA| damage, and this induction requires MEC1, a homolog of the ataxia telangiectasia mutated (ATM) |gene| . |DNA| damage-specific induction of HUG1, which is independent of the cell cycle stage, is due to the alleviation of repression by the Crt1p-Ssn6p-Tup1p complex. Overexpression of HUG1 is lethal in combination with a mec1 mutation in the presence of |DNA| damage or replication arrest, whereas a deletion of HUG1 rescues the lethality due to a mec1 null allele. HUG1 is the first example of a |NORF| with important biol. functional properties and defines a novel component of the MEC1 checkpoint pathway.
RE.CNT 55
RE
(1) Aboussekhra, A; EMBO J 1996, V15, P3912 CAPLUS
(2) Allen, J; Genes Dev 1994, V8, P2401 CAPLUS
(4) Basrai, M; Genome Res 1997, V7, P768 CAPLUS
(5) Basrai, M; Mol Cell Biol 1996, V16, P2838 CAPLUS
(6) Baudin, A; Nucleic Acids Res 1993, V21, P3329 CAPLUS
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L8 ANSWER 23 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:613552 CAPLUS
DN 131:306874
TI Suppression of AP-1 activity by tanshinone and cancer cell growth inhibition
AU Park, Seyeon; Song, Ji-Sung; Lee, Dug-Keun; Yang, Chul-Hak CS Department of Chemistry, Seoul National University, Seoul, 151-742, S. Korea
SO Bull. Korean Chem. Soc. (1999), 20(8), 925-928
CODEN: BKCSDE; ISSN: 0253-2964
PB Korean Chemical Society
DT Journal
LA English
AB The process of transcription is the major point at which |gene| expression is regulated. The jun and fos families of eukaryotic transcription factor heterodimerize to form complexes capable of binding 5'-TGAGTCA-3' |DNA| elements (AP-1 binding site). To search for the inhibitors of the jun-fos- |DNA| complex formation, several natural products exts. were screened and methanol ext. of tanshen (the dried roots of Salvia miltiorrhiza Bunge) showed remarkable inhibitory activity. The active compds. of the exts. were purified using repeated column chromatog. and recrystn. Their structures were identified as tanshinone I and tanshinone IIA. Through the electrophoresis mobility shift assay and cell cytotoxicity test, tanshinone I and tanshinone IIA were identified as inhibitors that suppress not only AP-1 function but also the cell proliferation.

Tanshinone I also suppressed the jun-fos- |DNA| complex formation in TPA-induced NIH 3T3 cells. RE.CNT 24
RE
(1) Angel, P; Biochim Biophys Acta 1991, V1072, P129 CAPLUS (2) Angel, P; Cell 1987, V49, P729 CAPLUS
(3) Angel, P; Cell 1988, V55, P875 CAPLUS
(4) Curran, T; Cell 1988, V55, P395 CAPLUS
(6) Greenberg, M; Nature 1984, V311, P433 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 24 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:606569 CAPLUS
DN 131:297269
TI Human endothelial cell life extension by telomerase expression AU Yang, Jiwei; Chang, Edwin; Cherry, Athena M.; Bangs, Charles D.; Oei, Yoko; Bodnar, Andrea; Bronstein, Adrienne; Chiu, Choy-Pik; Herron, G. Scott
CS Department of Dermatology, Stanford University School of Medicine, Stanford, CA, 94305-5486, USA
SO J. Biol. Chem. (1999), 274(37), 26141-26148
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology DT Journal
LA English
AB Normal human endothelial cells, like other somatic cells in culture, divide a limited no. of times before entering a nondividing state called replicative senescence. Expression of the catalytic component of human telomerase, human telomerase reverse transcriptase (hTERT), extends the life span of human fibroblasts and retinal pigment epithelial cells beyond senescence without causing neoplastic transformation (Bodnar, A. G., Ouellette, M., Frolkis, M., Holt, S. E., Chiu, C. P., Morin, G. B., Harley, C. B., Shay, J. W., Lichtsteiner, S., and Wright, W. E. (1998) Science 279, 349-352; Jiang, X., Jimenez, G., Chang, E., Frolkis, M., Kusler, B., |Sage| , M., Beeche, M., Bodnar, A., Wahl, G., Tlsty, T., and Chiu, C.-P. (1999) Nat. |Genet| . 21, 111-114). Here, we show that both human large vessel and microvascular endothelial cells also bypass replicative senescence after introduction of hTERT. For the first time, we report that hTERT expression in these life-extended vascular cells does not affect their differentiated and functional phenotype and that these cells maintain their angiogenic potential in vitro. Furthermore, hTERT(+) microvascular endothelial cells have normal karyotype, and hTERT(+) endothelial cell strains do not exhibit a transformed phenotype. Relative to parental cells at senescence, hTERT-expressing endothelial cells exhibit resistance to induction of apoptosis by a variety of different conditions. Such characteristics are highly desirable for designing vascular transplantation and |gene| therapy delivery systems in vivo.
RE.CNT 78
RE
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(6) Brooks, P; Cell 1994, V79, P1157 CAPLUS
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(8) Campisi, J; Cell 1996, V84, P497 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 25 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:593330 CAPLUS
DN 132:132840
TI Use of |cDNA| representational difference analysis to identify disease-specific |genes| in human atherosclerotic plaques AU Tyson, Kerry; Shanahan, Catherine
CS Department of Medicine, Addenbrooke's Hospital, University of Cambridge, Cambridge, UK
SO Methods Mol. Med. (1999), 30(Vascular Disease: Molecular Biology and Gene Therapy Protocols), 83-98
CODEN: MMMEFN
PB Humana Press Inc.
DT Journal
LA English
AB A PCR-based technique, |cDNA| representational difference anal. (|cDNA| RDA), is described that allows isolation of disease-specific clones using only microgram quantities of |RNA| . RDA of |cDNA| is a pos. selection technique that couples subtractive hybridization to PCR amplification, an approach that has several advantages over differential display RT-PCR and serial anal. of |gene| expression (|SAGE|). First, only sequences that are differentially expressed are amplified, avoiding the need for comparison of PCR fragments and reducing the isolation of false-pos. clones. Second, the subtractive hybridization steps generate a difference product representing all of the differentially expressed |genes| that are amplified in a single reaction. In addn., unwanted difference products can be eliminated during the hybridization step. Furthermore, the fragments generated by RDA are more likely to include sequences derived from the open reading frame of the |cDNA| , facilitating the identification of clones and providing useful information for novel |cDNAs| . Finally, |cDNA| RDA allows the isolation of clones representing rarely expressed |mRNAs| , and has been used to clone differentially expressed |genes| from a variety of systems. Exptl. protocols are provided for using |cDNA| RDA to isolate differentially expressed |genes| from human atherosclerotic plaques using only minimal amts. of total cytoplasmic |RNA| . RE.CNT 23
RE
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(3) Duguid, J; Proc Natl Acad Sci 1988, V85, P5738 CAPLUS
(4) Gonzalez-Zulueta, M; J Neurosci 1998, V18, P2040 CAPLUS (5) Gress, T; Genes Chromosomes and Cancer 1997, V19, P97 CAPLUS (6) Gubler, U; Gene 1983, V25, P263 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 26 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:553241 CAPLUS
DN 131:165790
TI Serial analysis of |gene| expression and its use to study |gene| expression in yeast and cancer cells
AU Velculescu, Victor E.
CS Johns Hopkins Univ., Baltimore, MD, USA
SO (1999) 91 pp. Avail.: UMI, Order No. DA9920791
From: Diss. Abstr. Int., B 1999, 60(3), 965
DT Dissertation
LA English
AB Unavailable

L8 ANSWER 27 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:494080 CAPLUS
DN 131:255349
TI Serial analysis of |gene| expression in human monocyte-derived dendritic cells
AU Hashimoto, Shin-Ichi; Suzuki, Takuji; Dong, Hong-Yan; Nagai, Shigenori; Yamazaki, Nobuyuki; Matsushima, Kouji
CS Department of Molecular Preventive Medicine and CREST, School of Medicine, The University of Tokyo, Tokyo, 113-0033, Japan
SO Blood (1999), 94(3), 845-852
CODEN: BLOOAW; ISSN: 0006-4971
PB W. B. Saunders Co.
DT Journal
LA English
AB Dendritic cells (DCs) are professional antigen-presenting cells in the immune system and can be generated in vitro from hematopoietic progenitor cells in the bone marrow, CD34+ cord blood cells, precursor cells in the peripheral blood, and blood monocytes by culturing with granulocyte-macrophage colony-stimulating factor (GM-CSF), interleukin-4, and tumor necrosis factor-.alpha.. The authors have performed serial anal. of |gene| expression (|SAGE|) in DCs derived from human blood monocytes. A total of 58,540 tag sequences from a DC |cDNA| library represented more than 17,000 different |genes| , and these data were compared with |SAGE| anal. of tags from monocytes (Mo) and GM-CSF-induced macrophages (M.phi.). Many of the |genes| that were differentially expressed in DCs were identified as |genes| encoding proteins related to cell structure and cell motility. Interestingly, the highly expressed |genes| in DCs encode chemokines such as TARC, MDC, and MCP-4, which preferentially chemoattract Th2-type lymphocytes. Although DCs have been considered to be very heterogeneous, the identification of specific |genes| expressed in human Mo-derived DCs should provide candidate |genes| to define subsets of, the function of, and the maturation stage of DCs and possibly also to diagnose diseases in which DCs play a significant role, such as autoimmune diseases and neoplasms. This study represents the first extensive |gene| expression anal. in any type of DCs. RE.CNT 29
RE
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 28 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:494079 CAPLUS
DN 131:270730
TI Serial analysis of |gene| expression in human monocytes and macrophages
AU Hashimoto, Shin-Ichi; Suzuki, Takuji; Dong, Hong-Yan; Yamazaki, Nobuyuki; Matsushima, Kouji
CS Department of Molecular Preventive Medicine and CREST, School of Medicine, The University of Tokyo, Tokyo, 113-0033, Japan
SO Blood (1999), 94(3), 837-844
CODEN: BLOOAW; ISSN: 0006-4971
PB W. B. Saunders Co.
DT Journal
LA English
AB Monocytes/macrophages serve as sentinels involved in chronic inflammation and the eradication of various pathogens. To define molecularly the differentiation of blood monocytes into macrophages, we conducted serial anal. of |gene| expression (|SAGE|) in human blood monocytes/macrophages induced by granulocyte-macrophage colony-stimulating factor (GM-CSF) or M-CSF. |SAGE| anal. of 57,560, 57,463, and 55,856 tags from monocytes, GM-CSF-, and M-CSF-induced macrophages, resp., allowed identification of 35,037 different transcripts. Interestingly, the |genes| with the highest expression during differentiation from monocytes into macrophages were |genes| involved in lipid metab. Both CSF-induced macrophages expressed similar sets of |genes| except for several |genes| such as monocyte-derived chemokine (MDC), legumain, prostaglandin D synthetase, and lysosomal sialoglycoprotein. The identification of specific |gene| expression in human monocytes, GM-CSF-, or M-CSF-induced macrophages provides novel methods to define macrophage subsets and the maturation and activation stage of cells of macrophage lineage and, possibly, to diagnose diseases in which macrophages play a major role. This study represents the first extensive serial anal. of |gene| expression for any type of human hematopoietic cells.
RE.CNT 32
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(4) Boot, R; J Biol Chem 1995, V270, P26252 CAPLUS
(5) Cecchini, M; Development 1994, V120, P1357 CAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 29 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:422148 CAPLUS
DN 131:306907

TI Effects of Salvia militorrhizae extract on endothelin and calcitonin |gene| -related peptide in chronic primary glomerulonephritis AU Wu, Yusheng; Yang, Jianhui; Jiang, Liping
CS Jinan Military General Hospital of PLA, Jinan, 250031, Peop. Rep. China SO Zhongguo Yiyuan Yaoxue Zazhi (1999), 19(5), 264-265
CODEN: ZYYAEP; ISSN: 1001-5213
PB Zhongguo Yiyuan Yaoxue Zazhi Bianjibu
DT Journal
LA Chinese
AB Patients with chronic primary glomerulonephritis (CPP) were divided into 2 groups: (1) those given the usual treatment with drugs and Chinese medicines; (2) those given the usual medicines plus S. militorrhizae ext. Plasma endothelin (ET) and calcitonin |gene| -related peptide (CGRP) levels were analyzed before and after treatment. The ET of CPP patients was higher, and that of CGRP was lower, than those in healthy subjects. The changes of ET and CGRP after treatment were significant in both groups, but the improvement in group 2 was better than that in group 1. Thus, S. militorrhizae was able to improve the imbalance of ET and CGRP in patients with CPP.

L8 ANSWER 30 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:411656 CAPLUS
DN 131:183979
TI Antioxidant actions of plant foods: use of oxidative |DNA| damage as a tool for studying antioxidant efficacy
AU Aruoma, Okezie I.
CS Faculty of Pharmaceutical Sciences, University of Sao Paulo-Ribeirao Preto, Ribeirao Preto-Sao Paulo, CEP 14040-903, Brazil SO Free Radical Res. (1999), 30(6), 419-427
CODEN: FRARER; ISSN: 1071-5762
PB Harwood Academic Publishers
DT Journal; General Review
LA English
AB A review with 40 refs. Plant-food-derived antioxidants and active principles such as flavonoids, hydroxycinnamates (ferulic acid, chlorogenic acids, vanillin etc.), .beta.-carotene and other carotenoids, vitamin E, vitamin C, or rosemary, |sage| , tea and numerous exts. are increasingly proposed as important dietary antioxidant factors. In this endeavor, assays involving oxidative |DNA| damage for characterizing the potential antioxidant actions are suggested as in vitro screens of antioxidant efficacy. The crit. question is the bioavailability of the plant-derived antioxidants.
RE.CNT 40
RE
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L8 ANSWER 31 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:407812 CAPLUS
DN 131:225251
TI Molecular biology and enzyme mechanisms of monoterpene synthases from culinary |sage| (Salvia officinalis)
AU Wise, Mitchell L.; Croteau, Rodney
CS Institute of Biological Chemistry, Washington State University, Pullman, WA, USA
SO Nat. Prod. Anal., [Symp.] (1998), Meeting Date 1997, 299-310. Editor(s): Schreier, Peter. Publisher: Vieweg, Wiesbaden, Germany. CODEN: 67USA7
DT Conference; General Review
LA English
AB A review with 33 refs. Studies on the biosynthesis of monoterpenes during the past two decades have provided a detailed understanding of the mechanisms, as well as the regio- and stereochem., by which the universal precursor, geranyl diphosphate, is converted to the various cyclic monoterpenes. Only through the use of cell free systems contg. the target, native enzymes have these biochem. characterizations been possible. However, as yet, relatively little is known about how the relevant enzymes channel the substrate into the appropriate conformation to facilitate cyclization or how they stabilize the highly reactive carbocationic intermediates through the reaction coordinate to the termination step. In order to assess these questions, and others pertaining to the structure and activity of these biocatalysts, the tools of mol. biol. are now being applied. In this report, the cloning and heterologous expression of three distinct monoterpene cyclases from culinary |sage| (Salvia officinalis), (+)-bornyl diphosphate synthase, 1,8-cineole synthase, and sabinene synthase, are described. All three of these recombinant enzymes produce multiple products from geranyl diphosphate. The implications of these product profiles for the corresponding reaction mechanisms will be described. The cloned |cDNAs| for these enzymes encode "pre-proteins" contg. a putative plastidial targeting peptide. Comparison of the amino acid sequences of these three cyclases from the same species, as well as sequence data from other monoterpene cyclases, has led to the identification of a tandem pair of absolutely conserved arginine residues. In the case of limonene synthase from spearmint (Mentha spicata), these tandem arginines represent the minimal cleavage site for a fully functional ("pseudomature") enzyme. The availability of several monoterpene cyclase |cDNA| clones from the same species presents an opportunity to compare amino acid sequence similarity without the ambiguities of interspecific variability. Identification of potentially significant motifs in the various cyclases, as well as prospects for

bioengineering of these enzymes, was discussed. RE.CNT 33
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(4) Back, K; Arch Biochem Biophys 1994, V315, P527 CAPLUS
(5) Bohlmann, J; J Biol Chem 1997, P21784 CAPLUS
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L8 ANSWER 32 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:395852 CAPLUS
DN 131:212926
TI High expression of the CC chemokine TARC in Reed-Sternberg cells: A possible explanation for the characteristic T-cell infiltrate in Hodgkin's lymphoma
AU Van den Berg, A.; Visser, L.; Poppema, S.
CS Department of Pathology and Laboratory Medicine, University Hospital Groningen, Groningen, 9700 RB, Neth.
SO Am. J. Pathol. (1999), 154(6), 1685-1691
CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal
LA English
AB Hodgkin's lymphoma is characterized by the combination of Reed-Sternberg (R-S) cells and a prominent inflammatory cell infiltrate. One of the intriguing questions regarding this disease is what is causing the influx of T lymphocytes into the involved tissues. The authors applied the serial anal. of |gene| expression (|SAGE|) technique on the Hodgkin's lymphoma-derived cell line L428 and on an Epstein-Barr virus (EBV)-transformed lymphoblastoid B-cell line. A frequently expressed tag in L428 corresponded to the T-cell-directed CC chemokine TARC. Reverse transcription polymerase chain reaction analyses demonstrated expression of TARC in nodular sclerosis (NS) and mixed cellularity (MC) classical Hodgkin's lymphomas but not in NLP Hodgkin's lymphoma, anaplastic large-cell lymphomas, and large-B-cell lymphomas with CD30 positivity. Two of 5 cases of T-cell-rich B-cell lymphoma (TCRBCL) were TARC pos. |RNA| in situ hybridization (ISH) showed a strong signal for TARC in the cytoplasm of R-S cells, and immunohistochem. staining confirmed the presence of the TARC protein in the R-S cells of NS and MC Hodgkin's lymphomas. The lymphocytic and histiocytic (L&H)-type cells of nodular lymphocyte predominance Hodgkin's lymphoma and the neoplastic cells of non-Hodgkin's lymphomas with the exception of 2 cases of TCRBCL did not stain for TARC. TARC is known to bind to the CCR4 receptor, which is expressed on activated Th2 lymphocytes. The immunophenotype of lymphocytes surrounding R-S cells is indeed Th2-like, and by |RNA| ISH these lymphocytes showed a pos. signal for the chemokine receptor CCR4. Thus, prodn. of TARC by the R-S cells may explain the characteristic T-cell infiltrate in classical Hodgkin's lymphoma. RE.CNT 25
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(2) Bargou, R; Blood 1996, V87, P4340 CAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 33 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:383651 CAPLUS
DN 131:115385
TI Production of lithospermic acid B and rosmarinic acid in hairy root cultures of Salvia miltiorrhiza
AU Chen, H.; Chen, F.; Zhang, Y-L.; Song, J-Y.
CS Department of Botany, The University of Hong Kong, Hong Kong, Hong Kong SO J. Ind. Microbiol. Biotechnol. (1999), 22(3), 133-138 CODEN: JIMBFL; ISSN: 1367-5435
PB Stockton Press
DT Journal
LA English
AB Hairy root cultures of Salvia miltiorrhiza were established by infecting sterile plantlets with Agrobacterium rhizogenes ATCC 15834, and the transformation was proved by direct detection of the inserted T- |DNA| by the polymerase chain reaction. As detd. by HPLC, these hairy root cultures had the ability to produce lithospermic acid B (LAB), rosmarinic acid (RA) and other related phenolic compds., the water-sol. active components of the plant. The effect of five different basal media, MS, MS-NH4 (MS without ammonium nitrate), B5, WPM and 6,7-V on the root growth and phenolic compd. prodn. was studied. It was found that MS-NH4 and 6,7-V media were superior to MS, B5 and WPM media in terms of both root growth and phenolic compd. prodn. The time course of biomass accumulation and phenolic compd. formation was also examd. in the culture using MS-NH4 medium. During cultivation, the content of RA in the roots was stable being approx. 0.48% of dry wt. while the content of LAB fluctuated between 0.73% and 1.61% of dry wt., and decreased gradually at the stationary phase of growth. The highest prodn. of LAB and RA was about 64 mg L-1 and 23 mg L-1, resp.
RE.CNT 37
RE
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L8 ANSWER 34 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:382552 CAPLUS
DN 131:155697
TI Dynamics of |gene| expression revealed by comparison of serial analysis of |gene| expression

transcript profiles from yeast grown on two different carbon sources
AU Kal, Arnoud J.; Van Zonneveld, Anton Jan; Benes, Vladimir; Van den Berg, Marlene; Koerkamp, Marian Groot; Albermann, Kaj; Strack, Normann; Ruijter, Jan M.; Richter, Alexandra; Dujon, Bernard; Ansorge, Wilhelm; Tabak, Henk F.
CS Dep. Biochem., Univ. Amsterdam, Amsterdam, 1105 AZ, Neth. SO Mol. Biol. Cell (1999), 10(6), 1859-1872
CODEN: MBCEEV; ISSN: 1059-1524
PB American Society for Cell Biology
DT Journal
LA English
AB A genome-wide characterization of |mRNA| transcript levels in yeast grown on the fatty acid oleate, detd. using Serial Anal. of |Gene| Expression (|SAGE|), is described. Comparison of this |SAGE| library with that reported for glucose-grown cells revealed the dramatic adaptive response of yeast to a change in C source. A major fraction (>20%) of the 15,000 |mRNA| mols. in a yeast cell comprised differentially expressed transcripts, which were derived from only 2% of the total no. of .apprx.6300 yeast |genes| . Most of the |mRNAs| that were differentially expressed code for enzymes or for other proteins participating in metab. (e.g., metabolite transporters). In oleate-grown cells, this was exemplified by the huge increase of |mRNAs| encoding the peroxisomal .beta.-oxidn. enzymes required for degrdn. of fatty acids. The data provide evidence for the existence of redox shuttles across organellar membranes that involve peroxisomal, cytoplasmic, and mitochondrial enzymes. The |mRNA| profile of a mutant strain with deletions of the PIP2 and OAF1 |genes| , encoding transcription factors required for induction of |genes| encoding peroxisomal proteins, also was analyzed. Induction of |genes| under the immediate control of these factors was abolished; other |genes| were up-regulated, indicating an adaptive response to the changed metab. imposed by the genetic impairment. A statistical method for anal. of data obtained by |SAGE| is described.
RE.CNT 45
RE
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(5) Audic, S; Genome Res 1997, V7, P986 CAPLUS
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L8 ANSWER 35 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:378408 CAPLUS
DN 131:29589
TI |DNA| degradation inhibitors containing pyroligneous acids, carbohydrates, and herbs
IN Takahashi, Masako; Kawase, Itsuko; Aki, Tatsuya
PA Apollo Yakkyoku Y. K., Japan; Hanaizumi Y. K.; Sanko K. K. SO Jpn. Kokai Tokkyo Koho, 3 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 11158001	A2	19990615	JP 1997-364237	19971128

AB The inhibitors, which prevents degrdn. of |DNA| used for |gene| therapy, |gene| synthesis, |gene| banks, genetic recombination, genetic engineering, etc., in medicine, agriculture, animal husbandry, and energy prodn., contain pyroligneous acids, carbohydrates, herbs, and herb exts. The inhibitors are esp. useful for preventing |DNA| degrdn. in tissues and cells fixed with formalin and diminishing toxicity of formalin. Sucrose, glucose, maltose, trehalose, etc., are used as the carbohydrates, and rosemary, mint, |sage| , chamomile, thyme, etc., are used as the herbs. Human tissues such as brain, lungs, etc., were fixed with a neutral buffered formalin contg. the inhibitor for 10 days. |DNAs| extd. from the fixed prepns. had higher mol. wt. than those extd. from formalin or neutral buffered formalin contg. no inhibitor.

L8 ANSWER 36 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:353621 CAPLUS
DN 131:140450
TI Inventory of high-abundance |mRNAs| in skeletal muscle of normal men
AU Welle, Stephen; Bhatt, Kirti; Thornton, Charles A.
CS Departments of Medicine, University of Rochester, Rochester, NY, 14642, USA
SO Genome Res. (1999), 9(5), 506-513
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The serial anal. of |gene| expression (|SAGE|) method was used to generate a catalog of 53,875 short (14 base) expressed sequence tags from polyadenylated |RNA| obtained from vastus lateralis muscle of healthy young men. Over 12,000 unique tags were detected. The frequency of occurrence of each tag reflects the relative abundance of the corresponding |mRNA| . The |mRNA| species that were detected 10 or more times, each comprising .gtoreq.0.02% of the |mRNA| population, accounted for 64% of the |mRNA| mass but <10% of the total no. of |mRNA| species detected. Almost all of the abundant tags matched |mRNA| or EST sequences cataloged in GenBank. Mitochondrial transcripts accounted for .apprx.20% of the polyadenylated |RNA| . Transcripts encoding proteins of the myofibrils were the most abundant nuclear-encoded |mRNAs| . Transcripts encoding ribosomal proteins, and those encoding proteins involved in energy metab., also were very abundant. The database can be used as a ref. for investigations of alterations in |gene| expression assocd. with conditions that influence muscle function, such as muscular dystrophies, aging, and exercise.
RE.CNT 18

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L8 ANSWER 37 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:321459 CAPLUS
DN 131:111925
TI Novel methods of |gene| expression pattern analysis
AU Feng, Wen-Zheng; Cao, Zhu-An; Liu, Jin-Yuan
CS School of Life Science and Engineering, Tsinghua University, Beijing, 100084, Peop. Rep. China
SO Shengwu Huaxue Yu Shengwu Wuli Jinzhan (1999), 26(2), 127-131 CODEN: SHYCD4; ISSN: 1000-3282
PB Shengwu Huaxue Yu Shengwu Wuli Jinzhan Bianjibu
DT Journal; General Review
LA Chinese
AB In the progress of the genome projects, the most important purpose of mol. biol. of the |gene| is to investigate the structure and function of not only individual important |genes| but also the whole genome, and the |gene| transcription and expression patterns of the whole cell. Serial anal. of |gene| expression (|SAGE|), |cDNA| microarray, |DNA| microchips for fast and quant. anal. of |gene| characteristics are reviewed with 13 refs.
L8 ANSWER 38 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:294028 CAPLUS
DN 131:56237
TI The periplasmic nitrate reductase in Pseudomonas sp. strain G-179 catalyzes the first step of denitrification
AU Bedzyk, Laura; Wang, Tao; Ye, Rick W.
CS DuPont Central Research and Development, Wilmington, DE, 19880-0328, USA SO J. Bacteriol. (1999), 181(9), 2802-2806
CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Both membrane-bound and periplasmic nitrate reductases have been found in denitrifying bacteria. Yet the role of periplasmic nitrate reductase in denitrification has not been clearly defined. To analyze the function of the periplasmic nitrate reductase in Pseudomonas sp. strain G-179, the nap |gene| cluster was identified and found to be linked to |genes| involved in redn. of nitrite and nitric oxide and anaerobic heme biosynthesis. Mutation in the nap region rendered the cells incapable of growing under anaerobic conditions with nitrate as the alternative electron acceptor. No nitrate redn. activity was detected in the Nap- mutant, but that activity could be restored by complementation with the nap region. Unlike the membrane-bound nitrate reductase, the nitrate redn. activity in strain G-179 was not inhibited by a low concn. of azide. Nor could it use NADH as the electron donor to reduce nitrate or use chlorate as the alternative substrate. These results suggest that the periplasmic nitrate reductase in this strain plays a primary role in dissimilatory nitrate redn.
RE.CNT 29
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 39 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:171055 CAPLUS
DN 131:14589
TI MicroSAGE: a modified procedure for serial analysis of |gene| expression in limited amounts of tissue
AU Datson, N. A.; Van der Perk-de Jong, J.; Van den Berg, M. P.; De Kloet, E. R.; Vreugdenhil, E.
CS Division of Medical Pharmacology, Leiden/Amsterdam Center for Drug Research, Leiden University, Leiden, 2300 RA, Neth.
SO Nucleic Acids Res. (1999), 27(5), 1300-1307
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Serial Anal. of |Gene| Expression (|SAGE|) is a powerful expression profiling method, allowing the anal. of the expression of thousands of transcripts simultaneously. A disadvantage of the method, however, is the relatively high amt. of input |RNA| required. Consequently, |SAGE| cannot be used for the generation of expression profiles when |RNA| is limited, i.e. in small biol. samples such as tissue biopsies or microdissected material. Here we describe a modification of |SAGE| , named microSAGE, which requires 500-5000-fold less starting material. Compared with |SAGE| , microSAGE is simplified due to incorporation of a "single-tube" procedure for all steps from |RNA| isolation to tag release. Furthermore, a limited no. of addnl. PCR cycles are performed. Using microSAGE |gene| expression profiles can be obtained from minute quantities of tissue such as a single hippocampal punch from a rat brain slice of 325 .mu.m thickness, estd. to contain, at most, 105 cells. This method opens up a multitude of new possibilities for the application of |SAGE| , for example the characterization of expression profiles in tissue biopsies, tumor metastases or in other cases where tissue is scarce and the generation of region-specific expression profiles of complex heterogeneous tissues.
RE.CNT 30
RE
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 40 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:170134 CAPLUS
DN 131:13491
TI Effects of Limonene, salvia miltiorrhiza and turmeric derivatives on H-ras oncogene expression and gap junction intercellular communication in human solid tumor cell lines
AU Chen, Xiaoguang; Hasuma, Tadayoshi; Yano, Yoshihisa; Yoshimata, Toshiko; Kamoi, Hiyoshi; Otani, Shuzo
CS Department of pharmacology, Institute of Materia Medica, Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing, 100050, Peop. Rep. China
SO Chin. J. Cancer Res. (1998), 10(3), 162-168
CODEN: CJCRFH; ISSN: 1000-9604
PB Chinese Journal of Cancer Research
DT Journal
LA English
AB We studied gap junction intercellular communication (GJIC), H-ras oncogene expression and ras oncogene product (P21 ras protein) expression in four human solid tumor cell lines, W1-38, CACO2, A549 and PaCa, and the effects of four compds., Salvia miltiorrhiza deriv. (SMD), d-Limonene, Turmeric deriv. I (TD-I) and Turmeric deriv. II (TD-II), on them. The abilities of the four solid tumor cell lines to transfer dye to adjacent cells were examd. by the scrape-loading/dye transfer technique, and the H-ras oncogene expression by Northern blotting and P21 ras protein expression by Western blotting. The results showed the loss of intercellular coupling in PaCa cells, slight GJIC in A549 and CACO2 cells, and a good GJIC in W1-38 cells. The four compds. could improve the GJIC of PaCa to different extents. The amt. of total and membrane assocd. P21 ras in PaCa cells were decreased after treatment with SMD, d-Limonene and TD-I (2.5 .mu.g/mL) for 48 h. Concomitantly, the growth of PaCa cells decreased in soft agar and had enhanced GJIC. The relative potency was found to be:d-Limonene>SMD >TD-I=TD-II. There was no significant effect of the four compds. on H-ras oncogene expression. It was suggested that there was an excellent correlation between loss of Lucifer Yellow dye transfer and ras |gene| mutation rate in the four solid tumor cell lines (ras |gene| mutation rate inversely correlated with av. cell no. coupled, r=0.98) i.e., the high ras |gene| mutation was closely correlated with loss of GJIC in these malignant human tumor cells;. The antitumor effect of the monoterpene d-Limonene and the phenol compd., SMD, might be related to inhibition of P21 ras membrane assocn. and enhancement of GJIC, while that of the others may be by a different mechanism;. The inhibition of P21 ras membrane assocn. was directly related to the enhancement of gap junction intercellular communication. RE.CNT 22
RE
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(4) Croteau, R; Chem Rev 1987, V87, P929 CAPLUS
(5) Crow, D; Mol Cell Biol 1990, V10, P1754 CAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 41 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:153949 CAPLUS
DN 130:293775
TI Correlation between protein and |mRNA| abundance in yeast AU Gygi, Steven P.; Rochon, Yvan; Franza, B. Robert; Aebersold, Ruedi CS Department of Molecular Biotechnology, University of Washington, Seattle, WA, 98195-7730, USA
SO Mol. Cell. Biol. (1999), 19(3), 1720-1730
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB We have detd. the relationship between |mRNA| and protein expression levels for selected |genes| expressed in the yeast Saccharomyces cerevisiae growing at mid-log phase. The proteins contained in total yeast cell lysate were sepd. by high-resoln. two-dimensional (2D) gel electrophoresis. Over 150 protein spots were excised and identified by capillary liq. chromatog.-tandem mass spectrometry (LC-MS/MS). Protein spots were quantified by metabolic labeling and scintillation counting. Corresponding |mRNA| levels were calcd. from serial anal. of |gene| expression (|SAGE|) frequency tables (V. E. Velculescu, L. Zhang, W. Zhou, J. Vogelstein, M. A. Basrai, D. E. Bassett, Jr., P. Hieter, B. Vogelstein, and K. W. Kinzler, Cell 88:243-251, 1997). We found that the correlation between |mRNA| and protein levels was insufficient to predict protein expression levels from quant. |mRNA| data. Indeed, for some |genes| , while the |mRNA| levels were of the same value the protein levels varied by more than 20-fold. Conversely, invariant steady-state levels of certain proteins were obsd. with resp. |mRNA| transcript levels that varied by as much as 30-fold. Another interesting observation is that codon bias is not a predictor of either protein or |mRNA| levels. Our results clearly delineate the tech. boundaries of current approaches for quant. anal. of protein expression and reveal that simple deduction from |mRNA| transcript anal. is insufficient. RE.CNT 40
RE
(1) Aebersold, R; Eur J Biochem 1986, V261, P4229 CAPLUS
(2) Aebersold, R; Proc Natl Acad Sci USA 1987, V84, P6970 CAPLUS (4) Bennetzen, J; J Biol Chem 1982, V257, P3026 CAPLUS

(5) Boucherie, H; Electrophoresis 1996, V17, P1683 CAPLUS
(6) Boucherie, H; Yeast 1995, V11, P601 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 42 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:136941 CAPLUS
DN 130:177973
TI Analysis of the entire |gene| expression by |SAGE|
AU Sasaki, Manabu; Nakahira, Kensuke; Ikenaka, Kazuhiro
CS Neural Inf., Natl. Inst. Physiol. Sci., Japan
SO Jikken Igaku (1999), 17(4), 497-502
CODEN: JIIGEF; ISSN: 0288-5514
PB Yodosha
DT Journal; General Review
LA Japanese
AB A review with 3 refs., on principle, procedure, and application of |SAGE| (serial anal. of |gene| expression).
L8 ANSWER 43 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:115534 CAPLUS
DN 130:292196
TI Substantially enhanced cloning efficiency of |SAGE| (Serial Analysis of |Gene| Expression) by adding a heating step to the original protocol
AU Kenzelmann, M.; Muhlemann, K.
CS Institute of Medical Microbiology, University of Bern, Bern, 3010, Switz. SO Nucleic Acids Res. (1999), 27(3), 917-918
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The efficiency of the original |SAGE| (Serial Anal. of |Gene| Expression) protocol was limited by a small av. size of cloned concatemers. We describe a modification of the technique that overcomes this problem. Ligation of ditags yields concatemers of various sizes. Small concatemers may aggregate and migrate with large ones during gel electrophoresis. A heating step introduced before gel electrophoresis breaks such contaminating aggregates. This modification yields cloned concatemers with an av. size of 67 tags as compared to 22 tags by the original protocol. It enhances the length of cloned concatemers substantially and reduces the costs of |SAGE| . RE.CNT 9
RE
(1) Bertelsen, A; Drug Discov Today 1998, V3, P152 CAPLUS
(2) Hermeking, H; Mol Cell 1997, V1, P3 CAPLUS
(3) Madden, S; Oncogene 1997, V15, P1079 CAPLUS
(4) Polyak, K; Nature 1997, V389, P300 CAPLUS
(5) Powell, J; Nucleic Acids Res 1998, V26, P3445 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 44 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:100739 CAPLUS
DN 130:149544
TI Serial analysis of |gene| expression method for rapid quantitative and qualitative analysis of transcripts
IN Kinzler, Kenneth W.; Vogelstein, Bert; Velculescu, Victor E.; Zhang, Lin PA The Johns Hopkins University School of Medicine, USA
SO U.S., 18 pp., Cont.-in-part of U.S. Ser. No. 527,154. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 5866330	A	19990202	US 1995-544861	19951018
US 5695937	A	19971209	US 1995-527154	19950912
EP 761822	A2	19970312	EP 1996-306634	19960912
EP 761822	A3	19980805		
R: AT, BE, CH, DE, DK, ES, FR, GR, IT, LI, NL, SE				
CA 2185379	AA	19970313	CA 1996-2185379	19960912
WO 9710363	A1	19970320	WO 1996-US14638	19960912
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
AU 9665614	A1	19970320	AU 1996-65614	19960912
AU 707846	B2	19990722		
AU 9670188	A1	19970401	AU 1996-70188	19960912
GB 2305241	A1	19970402	GB 1996-19024	19960912
GB 2305241	B2	19991110		
JP 10511002	T2	19981027	JP 1996-512103	19960912
PRAI US 1995-527154		19950912		
US 1995-544861		19951018		
WO 1996-US14638		19960912		

AB Serial anal. of |gene| expression, |SAGE| , a method for the rapid quant. and qual. anal. of transcripts is provided. Short defined sequence tags corresponding derived from |cDNAs| are isolated and ligated together to form dimerized tags, or ditags. By utilizing ditags, |SAGE| allows elimination of certain types of bias which might occur during cloning and/or amplification and possibly during data evaluation. Concatenation of these short nucleotide sequence tags allows the efficient anal. of transcripts in a serial manner by sequencing multiple tags on a single |DNA| mol, for example, a |DNA| mol. inserted in a vector or in a single clone. Sequencing of over 1000 defined tags in a short period of time (e.g., hrs.) reveals a |gene| expression pattern characteristics of the function of a cell or tissue. Moreover, |SAGE| is useful as a |gene| discovery tool for the identification in isolation of novel sequence tags corresponding to novel transcripts and |genes| . The method was applied to provide a qual. picture of |gene| expression in human pancreas, to quantify

levels of known pancreatic transcripts, and to identify novel pancreatic |genes| .
RE.CNT 33
RE
(1) Adams; Bioessays 1996, V18(4), P261 CAPLUS
(2) Adams; Nature 1992, V355, P632 CAPLUS
(3) Adams; Nature 1992, V355, P632 CAPLUS
(4) Adams; Science 1991, V252, P1651 CAPLUS
(6) Anon; WO 9300353 1993 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 45 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:90817 CAPLUS
DN 130:263052
TI Serial analysis of |gene| expression to assess the endothelial cell response to an atherogenic stimulus
AU De Waard, Vivian; Van den Berg, Birgit M. M.; Veken, Jeroen; Schultz-Heienbrok, Robert; Pannekoek, Hans; Van Zonneveld, Anton-Jan CS Department of Biochemistry, Academic Medical Center, University of Amsterdam, Amsterdam, 1105 AZ, Neth.
SO Gene (1999), 226(1), 1-8
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB Activation of human, arterial endothelial cells (ECs) is an early event in the pathogenesis of atherosclerosis. To identify the repertoire of |genes| that are differentially expressed after activation, we used serial anal. of |gene| expression (|SAGE|) to compare the |mRNA| spectrum of quiescent ECs with that of ECs activated for 6 h with a strong atherogenic stimulus. |SAGE| methodol. generates concatenated 'tags' of 10 bp that are derived from a specific |mRNA| . About 5% of over 12 000 tags analyzed is derived from |genes| that are differentially expressed (at least 5-fold up- or downregulated). These transcript tags are derived from only 56 |genes| , close to 1% of the total no. of analyzed |genes| . Among these 56 differentially expressed |genes| are 42 known |genes| , including the hallmark endothelial cell activation markers interleukin 8 (IL-8), monocyte chemoattractant protein 1 (MCP-1), vascular cell adhesion mol. 1 (VCAM-1), plasminogen activator inhibitor 1 (PAI-1), Gro-.alpha., Gro-.beta. and E-selectin. Differential transcription of a selection of the upregulated |genes| was confirmed by Northern blot anal. A novel observation is the upregulation of activin .beta.A |mRNA| , a member of the transforming growth factor .beta. family. Apparent discrepancies between this novel technol. and conventional methods are discussed. In conclusion, we demonstrate that for the application of |SAGE| , a moderate no. of analyzed transcript tags suffices to reveal the significant alterations of EC transcription that results from a strong atherogenic stimulus.
RE.CNT 33
RE
(1) Adams, M; Nature 1995, V377, P3 CAPLUS
(2) Bevilacqua, M; Science 1989, V243, P1160 CAPLUS
(4) Brand, K; J Clin Invest 1996, V97, P1715 CAPLUS
(5) Carmeliet, P; Circulation 1997, V96, P3180 CAPLUS
(6) Collins, T; Lab Invest 1993, V68, P499 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 46 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:88958 CAPLUS
DN 131:281
TI Effect of d-limonene, Salvia miltiorrhiza and turmeric derivatives on membrane association and gap junction intercellular communication of ras |gene| product
AU Chen, Xiaoguang; Shuzo, Otani; Li, Yan; Han, Rui
CS Institute of Materia Medica, Chinese Academy of Medical Sciences, Peking Union Medical College, Beijing, 100050, Peop. Rep. China SO Yaoxue Xuebao (1998), 33(11), 821-827
CODEN: YHHPAL; ISSN: 0513-4870
PB Chinese Academy of Medical Sciences, Institute of Materia Media DT Journal
LA Chinese
AB Gap junction intercellular communication (GJIC), H-ras oncogene expression and Ras oncogene product (P21ras protein) expression were studied in 4 human solid tumor cell lines, W1-38, CACO2, A549 and PaCa (with the different Ras |gene| mutation rate), and the effects on them of an active compd. of Salvia miltiorrhiza (SMD), d-limonene, curcumine turmeric deriv. I (TD-I) and II were obsd. The abilities of the 4 solid tumor cell lines to transfer dye to adjacent cells were examd. using the scrape-loading/dye transfer technique, and the H-ras oncogene expression by Northern blotting and P21ras protein expression by Western blotting. The results showed that the loss of the function of dye transfer in cell was pos. with the mutation rate of ras |gene| . The anticancer activity of SMD and d-limonene might be related with inhibition of membrane assocn. of P21ras protein and the increase of gap junction intercellular communication. The relative potency was: d-limonene > SMD > TD-I = TD-II. No significant effect of these 4 compds. on H-ras oncogene expression was obsd.

L8 ANSWER 47 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:53128 CAPLUS
DN 130:247494
TI |Gene| expression informatics-it's all in your mine
AU Bassett, Douglas E., Jr; Eisen, Michael B.; Boguski, Mark S. CS Rosetta Inpharmatics, Kirkland, WA, 98034, USA
SO Nat. Genet. (1999), 21(1, Suppl.), 51-55
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal; General Review
LA English
AB A review with 37 refs. that discusses some of the tech. and intellectual issues involved in taking the vast amt. of information obtained from whole-genome |RNA| expression studies and making it more suitable

for comparative anal. and for inter-operability with other information resources. The review also addresses how the information is currently being organized and provides some thoughts about future directions. Currently, there are limited no. of efficient, publically available tools for data processing, storing and retrieving information and for analyzing the results in the context of existing knowledge. In addn., there is no consensus on how to compare the results using different technologies (for example, microarrays vs. oligonucleotide chips vs. |SAGE|). There is also no consensus on who to communicate results using existing publication modalities and public database systems. Improved access to large electronic data sets, reliable and consistent annotation and effective tools for "data mining" are crit. Anal. methods that exploit large data warehouses of |gene| expression expts. will be necessary to realize the full potential of this technol. RE.CNT 37
RE
(2) Benson, D; Nucleic Acids Res 1998, V26, P1 CAPLUS
(4) Brown, P; Nature Genet 1999, V21, P33 CAPLUS
(5) Brownstein, M; Trends Guide to Bioinformatics 1998, P27 CAPLUS (7) Chen, Y; Biomed Optics 1997, V2, P364 CAPLUS
(8) Cheung, V; Nature Genet 1999, V21, P15 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 48 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:48825 CAPLUS
DN 130:134943
TI Determination of p53-controlled |genes| (via |SAGE|) and their uses in cancer diagnosis
IN Madden, Stephen L.; Galella, Elizabeth A.; Bertelsen, Arthur H.; Beaudry, Gary A.
PA Genzyme Corporation, USA
SO PCT Int. Appl., 32 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9901581	A1	19990114	WO 1998-US13903	19980702
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9883829	A1	19990125	AU 1998-83829	19980702
PRAI US 1997-51573		19970702		
WO 1998-US13903		19980702		

AB Rat embryo fibroblast (REF) cells were transformed with activated RAS and a mouse temp.-sensitive p53 (Val135) |gene| , thereby forming a tightly regulated, well defined system to study mechanisms involved in p53-mediated cell growth regulation. Serial anal. of |gene| expression (|SAGE|) allows for a quant., representative, and comprehensive profile of |gene| expression, and |SAGE| technol. was used in the invention to contrast the differential |gene| expression profile in REF cells producing temp.-sensitive p53 tumor suppressor protein. Anal. of .apprx.15,000 |genes| revealed that the expression of 14 |genes| was dependent on functional p53 protein, whereas the expression of 3 |genes| was significantly higher in cells producing non-functional p53 protein. The |genes| which are identified as being upregulated or downregulated by p53 can be used to diagnose cancer in a sample by detecting the level of transcription of an |RNA| mol. and comparing it to the level in a normal tissue of the same type. Also, a method is provided for evaluating the cytotoxicity or carcinogenicity of an agent.
RE.CNT 7
RE
(2) Buckbinder, L; Proceedings of the National Academy of Sciences of USA 1994, V91, P10640 CAPLUS
(3) Iotsova, V; Oncogene 1996, V13(11), P2331 CAPLUS
(4) Madden, S; Cancer Research 1996, V56(23), P5384 CAPLUS (5) Madden, S; Oncogene 1997, V15(9), P1079 CAPLUS
(6) Pharmagenics Inc; WO 9745542 A 1997 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 49 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:47343 CAPLUS
DN 130:205604
TI High throughput analysis of differential |gene| expression AU Carulli, John P.; Artinger, Michael; Swain, Pamela M.; Root, Colleen D.; Chee, Linda; Tulig, Craig; Guerin, Jennifer; Osborne, Mark; Stein, Gary; Lian, Jane; Lomedico, Peter T.
CS Dep. Human Genetics, Genome Therapeutics Corp., Waltham, MA, 02154, USA SO J. Cell. Biochem. (1998), (Suppl. 30/31), 286-296
CODEN: JCEBD5; ISSN: 0730-2312
PB Wiley-Liss, Inc.
DT Journal; General Review
LA English
AB A review with 33 refs. Elucidation of the changes in |gene| expression assocd. with biol. processes is a central problem in biol. Advances in mol. and computational biol. have led to the development of powerful, high-throughput methods for the anal. of differential |gene| expression. These tools have opened up new opportunities in disciplines ranging from cell and developmental biol. to drug development and pharmacogenomics. In this review, the attributes of five commonly used differential |gene| expression methods are discussed: expressed sequence tag (EST) sequencing, |cDNA| microarray hybridization, subtractive cloning, differential display, and serial anal. of |gene| expression (|SAGE|). The application of EST sequencing and microarray hybridization is illustrated by the discovery of novel |genes| assocd. with osteoblast differentiation. The application of subtractive cloning is presented as a tool to identify |genes| regulated in vivo by the transcription factor pax-6. These and other examples illustrate the power of genomics for discovering novel |genes| that are important in biol. and which also represent new

targets for drug development. The central theme of the review is that each of the approaches to identifying differentially expressed |genes| is useful, and that the exptl. context and subsequent evaluation of differentially expressed |genes| are the crit. features that det. success.
RE.CNT 33
RE
(2) Adams, M; Science 1991, V252, P1651 CAPLUS
(3) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(4) Altschul, S; Nucleic Acids Res 1997, V25, P3389 CAPLUS (5) Bonaldo, M; Genome Res 1996, V6, P791 CAPLUS
(6) Buckbinder, L; Proc Natl Acad Sci USA 1994, V91, P10640 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 50 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1999:2901 CAPLUS
DN 130:180813
TI Serial analysis of |gene| expression in non-small cell lung cancer AU Hibi, Kenji; Liu, Qing; Beaudry, Gary A.; Madden, Stephen L.; Westra, William H.; Wehage, Scott L.; Yang, Stephen C.; Heitmiller, Richard F.; Bertelsen, Arthur H.; Sidransky, David; Jen, Jin
CS Department of Otolaryngology-Head and Neck Surgery Division of Head and Neck Cancer Research, Johns Hopkins University School of Medicine, Baltimore, MD, 21205-2196, USA
SO Cancer Res. (1998), 58(24), 5690-5694
CODEN: CNREA8; ISSN: 0008-5472
PB AACR Subscription Office
DT Journal
LA English
AB The authors used the serial anal. of |gene| expression (|SAGE|) method to systematically analyze transcripts present in non-small cell lung cancer. Over 226,000 |SAGE| tags were sequence analyzed from two independent primary lung cancers and two normal human bronchial/tracheal epithelial cell cultures. A total of 226,000 |SAGE| tags were sequence identified, representing 43,254 unique transcripts. Comparison of the tags present in the tumor with those identified in the normal tissue revealed 175 transcript tags that were overrepresented in the normal tissue and 142 tags that were overexpressed in the tumor by 10-fold or more. Northern hybridization was performed on 15 of the most abundantly expressed tags identified in the tumors. These tags were derived from either a known |gene| or a matched expressed sequence tag clone. The transcripts for 3 of the 15 |genes| , PGP 9.5, B-myb, and human mutT, were abundantly expressed in primary lung cancers (10 of 18, 15 of 18, and 6 of 12 tumors, resp.). In contrast, the presence of PGP9.5 and B-myb was much less frequent in primary tumors derived from other tissue origins. These results suggest that at least a portion of the transcripts identified by |SAGE| are frequently assocd. with lung cancer, and that their overexpression may contribute to lung tumorigenesis. The identification and further characterization of |genes| generated by |SAGE| should provide potential new targets for the diagnosis, prognosis, and therapy of lung cancer.
RE.CNT 44
RE
(2) Arsura, M; Blood 1994, V83, P1778 CAPLUS
(5) DeRisi, J; Nat Genet 1996, V14, P457 CAPLUS
(6) Diehl, J; Genes Dev 1997, V11, P957 CAPLUS
(7) Gazdar, A; Anticancer Res 1994, V14, P261 CAPLUS
(9) Hermeking, H; Mol Cell 1997, V1, P3 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 51 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:744115 CAPLUS
DN 130:149114
TI Differential display of |mRNA|
AU Zhang, John S.; Duncan, Emma L.; Chang, Andy C.-M.; Reddel, Roger R. CS Children's Medical Research Institute, Sydney, NSW 2145, Australia SO Mol. Biotechnol. (1998), 10(2), 155-165
CODEN: MLBOEO; ISSN: 1073-6085
PB Humana Press Inc.
DT Journal; General Review
LA English
AB A review with 61 refs. on differential display of |mRNA| . Differential display of |mRNA| (DD) is a technique in which |mRNA| species expressed by a cell population are reverse transcribed and then amplified by many sep. polymerase chain reactions (PCR). PCR primers and conditions are chosen so that any given reaction yields a limited no. of amplified |cDNA| fragments, permitting their visualization as discrete bands following gel electrophoresis. This robust and relatively simple procedure allows identification of |genes| that are differentially expressed in different cell populations. DD is compared with other techniques for analyzing differential |mRNA| expression such as RDA (representational difference anal.), SSH (suppression subtractive hybridization), and |SAGE| (serial anal. of |gene| expression). RE.CNT 61
RE
(1) An, G; BioTechniques 1996, V20, P342 CAPLUS
(3) Averboukh, L; BioTechniques 1996, V20, P918 CAPLUS
(4) Bauer, D; Nucleic Acids Res 1993, V21, P4272 CAPLUS
(6) Callard, D; BioTechniques 1994, V16, P1096 CAPLUS
(7) Chang, A; Mol Cell Endocrinol 1995, V112, P241 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 52 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:649237 CAPLUS
DN 130:11086
TI A strategy for genome-wide |gene| analysis: integrated procedure for |gene| identification
AU Wang, San Ming; Rowley, Janet D.
CS Section of Hematology and Oncology, University of Chicago Medical Center, Chicago, IL, 60637-1470, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1998), 95(20), 11909-11914 CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences
DT Journal
LA English
AB We have developed a technique called the Integrated Procedure for |Gene| Identification that modifies and integrates parts from several existing techniques to increase the efficiency for genome-wide |gene| identification. The procedure has the following features: (1) Only the 3' portion of the expressed templates is used to ensure a match to 3' expressed sequence tag (EST) sequences; (2) the 3' portion of the |cDNA| is poly dA/poly dT minus, which maintains complete representation of the expressed copies, particularly the rare copies, which otherwise would be lost heavily because of random poly dA/poly dT hybridization in the subtraction reaction; (3) redundancy is decreased substantially by the subtraction reaction to reduce the effort for sequencing anal.; (4) the nonsubtracted templates that largely contain the rare copies are amplified selectively with suppression PCR and are sequenced directly or through serial anal. of |gene| expression (|SAGE|); and (5) the identified sequences are matched to databases to det. whether they are cloned |genes| , ESTs, or novel sequences. Using this procedure in a model system, we showed that the redundant copies were largely removed, and the rates of EST matches and the novel sequence identification were significantly increased. Most of the plasmids contg. the matched EST are readily available from the IMAGE consortium. This technique can be used to index genome-wide expressed |genes| and to identify differentially expressed |genes| in different cells. Compared with the existing techniques, this procedure is relatively efficient, simple, less expensive, and labor intensive. It is esp. useful for std. mol. labs. to perform genome-wide studies. RE.CNT 19
RE
(2) Bertling, W; PCR Methods Appl 1993, V3, P95 CAPLUS
(3) Bhattacharyya, T; J Biol Chem 1995, V270, P1705 CAPLUS (4) Boguski, M; Trends Biochem Sci 1995, V20, P295 CAPLUS
(5) Bonaldo, M; Genome Res 1996, V6, P791 CAPLUS
(6) DeRisi, J; Nat Genet 1996, V14, P457 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 53 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:637211 CAPLUS
DN 130:61623
TI |SAGE| (Serial Analysis of |Gene| Expression) AU Tazawa, Ryushi; Suzuki, Takuji
CS Aging Medicine Laboratory, Tohoku University, Japan
SO Bunshi Kokyukibyo (1998), 2(5), 373-375
CODEN: BUKOFC; ISSN: 1342-436X
PB Sentan Igakusha
DT Journal; General Review
LA Japanese
AB A review with 5 refs. on the principles and the procedure of |SAGE| (Serial Anal. of |Gene| Expression).

L8 ANSWER 54 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:547648 CAPLUS
DN 129:297789
TI Role of molecular biology in strategies to discover novel targets for drug development
AU Feuerstein, Giora Z.; Barone, Frank C.; Wang, Xinkang CS Department of Cardiovascular Pharmacology, SmithKline Beecham Pharmaceuticals, King of Prussia, PA, USA
SO New Front. Stress Res., [OHOLO Res. Conf.], 40th (1998), Meeting Date 1996, 285-293. Editor(s): Levy, Aharon. Publisher: Harwood, Amsterdam, Neth.
CODEN: 66NUA5
DT Conference; General Review
LA English
AB A review with many refs. The authors describe overall strategies for the discovery of disease/stress related |gene| expression, with special attention to |mRNA| differential display technique as an example for a successful application in a particular condition of brain injury, i.i., brain ischemia. While the example provided in this review is drawn from brain injury by a pathophysiol. condition (stroke), the method is applicable to all tissues and cells and therefore likely to be of great value also in stress research. Differential display is one of the most flexible and comprehensive methods available for the detection of differentially expressed |genes| in cells and tissues. Since its initial description, this technique has been established in many labs. and successfully applied for the identification of |genes| in in vitro and in vivo systems. Similarly, other methods, such as subtractive library screening, differential hybridization, |SAGE| and RDA have also been successfully used for novel |gene| discovery. The application of these techniques will no doubt facilitate the discovery of novel therapeutic targets and help increase the understanding of the mol. mechanisms of disease. The same strategies are also feasible for novel |gene| discovery in brain under stress conditions. However, this is the first of many steps required in the discovery of a novel pharmacol. target, esp. since the function of the novel |gene| is likely to be unknown. Therefore, further actions should be take to characterize the functions of the differentially expressed |gene| , including isolation of the full length |cDNA| , expression of the |gene| product for functional studies and target validation for the importance of this |gene| in the disease process.

L8 ANSWER 55 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:518514 CAPLUS
DN 129:212223
TI Enhanced concatemer cloning - a modification to the |SAGE| (Serial Analysis of |Gene| Expression) technique
AU Powell, J.
CS The Richard Dimbleby Department of Cancer Research, I.C.R.F. Laboratory, Rayne Institute, St Thomas's

Hospital, London, SE1 7EH, UK SO Nucleic Acids Res. (1998), 26(14), 3445-3446
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The Serial Anal. of |Gene| Expression (|SAGE|) method, described in 1995 by Velculescu et al., represents a powerful means to compare |gene| expression between two |mRNA| populations. An improvement to |SAGE| that removes contaminating linker mols., which compromise the efficiency of the method, has been developed. This modification utilizes biotinylated PCR primers, which generate biotinylated linkers at an early stage in the |SAGE| protocol, thus allowing removal of the unwanted linkers by binding to streptavidin-coated magnetic beads at a later stage. The application of this modification resulted in the rapid generation of high ditag yields and clones with large av. insert sizes.

L8 ANSWER 56 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:449034 CAPLUS
DN 129:199205
TI Detection of natural bioantimutagens and their mechanisms of action with bacterial assay-system
AU Simic, Draga; Vukovic-Gacic, Branka; Knezevic-Vukcevic, Jelena CS Faculty of Biology, Laboratory for Microbiology, University of Belgrade, Belgrade, 11000, Yugoslavia
SO Mutat. Res. (1998), 402(1,2), 51-57
CODEN: MUREAV; ISSN: 0027-5107
PB Elsevier Science B.V.
DT Journal
LA English
AB Escherichia coli K12 assay-system is designed in order to detect bioantimutagens, agents preventing mutagenesis by modulation of |DNA| repair and replication. The assay is composed of four tests aimed at the detection of inhibition of spontaneous and induced mutations (Tests A and B) and at the estn. whether the anti-mutagenic agent acts by increasing the fidelity of |DNA| replication (Test B), by inhibition of SOS error prone repair (Test C), or by favoring error-free recombinational repair (Test D). In Test A, repair proficient strain and its uvrA counterpart are used for detection of spontaneous and UV-induced mutations, while in Test B mismatch repair deficient strains (mutH, mutS, mutL and uvrD) are used for amplified detection of spontaneous mutations caused by replication errors. In Test C, repair proficient strain carrying sfiA:: lacZ fusion is used for measuring the level of SOS induction by monitoring the level of .beta.-galactosidase. In Test D, the strains carrying different recA alleles (recA+, recA730 and .DELTA.recA) are used for measuring intrachromosomal recombination between nonoverlapping deletions in duplicated lac operon, by monitoring Lac+ recombinants. The assay-system is validated with model bioantimutagens and used for detection of anti-mutagenic potential of different terpenoid fractions from |sage| (Salvia officinalis). Ext. E1/3 of cultivated |sage| , distinguished from others by its high content of monoterpenoid camphor, reduces UV-induced mutagenesis in Test A, while it has no effect in Tests B and C. In Test D, it enhances intrachromosomal recombination in untreated and UV-irradiated recA+ and recA730 strains. The results suggest that the protective effect is due to stimulation of recombinational repair, similarly to coumarin. We speculate that monoterpenoids from |sage| enhance genetic recombination by intervening in a formation of RecA- |DNA| complex and channeling it into recombination reaction.

L8 ANSWER 57 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:403160 CAPLUS
DN 129:146266
TI Monoterpene synthases from common |sage| (Salvia officinalis) |cDNA| isolation, characterization, and functional expression of (+)-sabinene synthase, 1,8-cineole synthase, and (+)-bornyl diphosphate synthase
AU Wise, Mitchell L.; Savage, Thomas J.; Katahira, Eva; Croteau, Rodney CS Institute of Biological Chemistry, and Department of Biochemistry and Biophysics, Washington State University, Pullman, WA, 99164-6340, USA SO J. Biol. Chem. (1998), 273(24), 14891-14899
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology DT Journal
LA English
AB Common |sage| (Salvia officinalis) produces an extremely broad range of cyclic monoterpenes bearing diverse carbon skeletons, including members of the p-menthane (1,8-cineole), pinane (a- and P-pinene), thujane (isothujone), camphane (camphene), and bornane (camphor) families. An homol.-based polymerase chain reaction cloning strategy was developed and used to isolate the |cDNAs| encoding three multiproduct monoterpene synthases from this species that were functionally expressed in Escherichia coli. The heterologously expressed synthases produce (+)-bornyl diphosphate, 1,8-cineole, and (+)-sabinene, resp., as their major products from geranyl diphosphate. The bornyl diphosphate synthase also produces significant amts. of (+)-.alpha.-pinene, (+)-camphene, and (t)-limonene. The 1,8.cineole synthase produces significant amts. of (+)- and (-)-.alpha.-pinene, (+)- and (-)-/-pinene, myrcene and (+)-sabinene, and the (+)-sabinene synthase produces significant quantities of .gamma.-terpinene and terpinolene. All three enzymes appear to be translated as preproteins bearing an amino-terminal plastid targeting sequence, consistent with the plastidial origin of monoterpenes in plants. Deduced sequence anal. and size exclusion chromatog. indicate that the recombinant bornyl diphosphate synthase is a homodimer, whereas the other two recombinant enzymes are monomeric, consistent with

the size and subunit architecture of their native enzyme counterparts. The distribution and stereochem. of the products generated by the recombinant (+)-bornyl diphosphate synthase suggest that this enzyme might represent both (+)-bornyl diphosphate synthase and (+)-pinene synthase which were previously assumed to be distinct enzymes.

L8 ANSWER 58 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:388688 CAPLUS
DN 129:66836
TI Method to detect IgE
IN Frank, Robert Glenn; Porter, James P.; Rushlow, Keith E.; Wassom, Donald L.
PA Heska Corporation, USA
SO PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9823964	A1	19980604	WO 1997-US21651	19971124

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

US 5945294 A 19990831 US 1996-756387 19961126 AU 9874114 A1 19980622 AU 1998-74114 19971124 EP 943097 A1 19990922 EP 1997-949625 19971124 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRAI US 1996-756387 19961126
WO 1997-US21651 19971124

AB The present invention includes a method to detect IgE using a human Fc epsilon receptor (Fc.epsilon.R) to detect IgE antibodies in a biol. sample from a cat, a dog, or a horse. The present invention also relates to kits to perform such methods. The kits comprise an allergen common to all regions of the United States and a human Fc.epsilon. receptor mol.

L8 ANSWER 59 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:251960 CAPLUS
DN 129:39746
TI Identification of human plasma kallikrein |gene| polymorphisms and evaluation of their role in end-stage renal disease
AU Yu, Hongrun; Bowden, Donald W.; Spray, Beverly J.; Rich, Stephen S.; Freedman, Barry I.
CS Dep. Biochem., Internal Med./Section Nephrol., Public Health Sci., Wake Forest Univ., Winston-Salem, NC, 27157-1053, USA
SO Hypertension (1998), 31(4), 906-911
CODEN: HPRTDN; ISSN: 0194-911X
PB Williams & Wilkins
DT Journal
LA English
AB Kallikreins are serine proteases that release kinins from kininogens. Kinins, via their effects on cardiovascular and renal function, may be involved in the pathogenesis of hypertension and renal failure. Two groups of kallikreins exist, glandular or tissue kallikrein and plasma kallikrein. In this study, the authors examd. the human plasma kallikrein |gene| KLK3 to det. whether it contributed to end-stage renal disease (ESRD) susceptibility. The authors identified two novel polymorphic sequences closely linked to the KLK3 |gene| , designated KLK3b and KLK3c (heterozygosities: 0.64 to 0.68 and 0.48 to 0.52, resp.). The authors mapped the KLK3 |gene| and the marker KLK3c to the long arm of human chromosome 4 between F11 and D4S426 using a radiation hybrid panel. The study population consisted of 142 sibling pairs concordant for ESRD from 121 African American families. The 142 sibling pairs were stratified into 78 pairs with hypertension- and chronic glomerulonephritis-assocd. ESRD and 64 with non-insulin-dependent diabetes mellitus-assocd. ESRD. Linkage analyses, using SIBPAL of |SAGE| , and exclusion anal., using MAPMAKERS/SIBS, were performed. Linkage anal. of affected sibling pairs did not reveal any evidence of linkage of KLK3 to ESRD in all 142 sib-pairs or in the two stratified subsets. Exclusion anal. indicated that the KLK3 |gene| could be excluded from contributing to ESRD at a relative risk of 3 when the max. log of the odds score of -2 was used as the criterion for exclusion. However, an assocn. anal. using the relative predispositional effect technique showed that alleles 7 and 9 of KLK3b were consistently assocd. with ESRD. Alleles 7 and 9 were present in 11.2% and 10.8% of the 113 unrelated ESRD probands and in 6.6% and 6.6% of the 204 race-matched control subjects without renal disease (allele and.0016, resp.). Alleles 7 and 9 were also present in 13% and 10.4% of the proband's first siblings (allele and.0087, resp.). The assocn. of KLK3b alleles with ESRD raises the possibility that polymorphisms in KLK3 may play a role in ESRD susceptibility. The lack of linkage might reflect the relatively small family set.

L8 ANSWER 60 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:249595 CAPLUS
DN 129:51247
TI Inhibition of |DNA| topoisomerase I by cryptotanshinone from Salvia miltiorrhiza
AU Lee, Dong-Sun; Hong, Soon-Duck
CS Department of Microbiology, College of Natural Science, Kyungpook National University, Taegu, 702-701, S. Korea
SO J. Microbiol. Biotechnol. (1998), 8(1), 89-91
CODEN: JOMBES; ISSN: 1017-7825
PB Korean Society for Applied Microbiology
DT Journal
LA English
AB Cryptotanshinone (I) induced |DNA| topoisomerase I (II)-mediated |DNA| cleavage in vitro as strongly as

camptothecin, whereas |DNA| topoisomerase II-mediated |DNA| cleavage was not induced by this agent. In a |DNA| relaxation assay using calf thymus II and supercoiled pBR322 |DNA| , I inhibited II-mediated |DNA| relaxation in a dose-dependent manner. In an unwinding assay, I (50 .mu.M) did not shift the topoisomers of |DNA| . These results suggest that I exerted a preferential inhibition of II without intercalating into |DNA| .

L8 ANSWER 61 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:241078 CAPLUS
DN 129:63524
TI High-throughput |gene| expression analysis using |SAGE| AU Bertelsen, Arthur H.; Velculescu, Victor E.
CS Schering Plough Research Institute, Kenilworth, NJ, 07033, USA SO Drug Discovery Today (1998), 3(4), 152-159
CODEN: DDTOFS; ISSN: 1359-6446
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review with 31 refs. The pharmaceutical industry has long been in search of new targets for drug development. A rational approach to the identification of relevant drug targets involves the characterization of |gene| products that participate in disease processes. The wealth of |DNA| data generated by the Human Genome Project has identified a substantial fraction of human |genes| , but has done little to elucidate their role in normal and disease states. One powerful method to reveal insights into |gene| function and |gene| pathways is the systematic anal. of |gene| expression profiles. Serial anal. of |gene| expression (|SAGE|) offers an efficient and comprehensive approach to |gene| expression anal. It has already been used to provide insights into the pathophysiol. of cancer and to open up possibilities for useful diagnostic and therapeutic interventions.

L8 ANSWER 62 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:168924 CAPLUS
DN 128:278731
TI Expression of angiostatin |cDNA| in a murine fibrosarcoma suppresses primary tumor growth and produces long-term dormancy of metastases
AU Cao, Yihai; O'reilly, Michael S.; Marshall, Blair; Flynn, Evelyn; Ji, Richard-Weidong; Folkman, Judah
CS Laboratory of Angiogenesis Research, Microbiology and Tumor Biology Center, Karolinska Institute, Stockholm, S-171 77, Swed. SO J. Clin. Invest. (1998), 101(5), 1055-1063
CODEN: JCINAO; ISSN: 0021-9738
PB Rockefeller University Press
DT Journal
LA English
AB Tumor growth and metastasis are angiogenesis dependent. Previously, the authors reported that angiostatin, a potent angiogenesis inhibitor, produced by a primary Lewis lung carcinoma suppressed its growth of lung metastases (O'Reilly, M.S., L. Holmgren, Y. Shing, C. Chen, R.A. Rosenthal, M. Moses, W.S. Lane, Y. Cao, E.H. |Sage| , and J. Folkman. 1994. Cell. 79:315-328). Now the authors show that a shift of balance of tumor angiogenesis by |gene| transfer of a |cDNA| coding for mouse angiostatin into murine T241 fibrosarcoma cells suppresses primary and metastatic tumor growth in vivo. Implantation of stable clones expressing mouse angiostatin in C57B16/J mice inhibits primary tumor growth by an av. of 77%. After removal of primary tumors, the pulmonary micrometastases in .apprx. 70% of mice remain in a microscopic dormant and avascular state for the duration of the expts., e.g., 2-5 mo. The tumor cells in the dormant micrometastases exhibit a high rate of apoptosis balanced by a high proliferation rate. The study, to the knowledge, for the first time shows the diminished growth of lung metastases after removal of the primary tumor, suggesting that metastases are self-inhibitory by halting angiogenesis. The data may also provide a novel approach for cancer therapy by antiangiogenic |gene| therapy with a specific angiogenesis inhibitor.

L8 ANSWER 63 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:168617 CAPLUS
DN 128:293580
TI Manganese superoxide dismutase protects nNOS neurons from NMDA and nitric oxide-mediated neurotoxicity
AU Gonzalez-Zulueta, Mirella; Ensz, Lisa M.; Mukhina, Galina; Lebovitz, Russell M.; Zwacka, Ralf M.; Engelhardt, John F.; Oberley, Larry W.; Dawson, Valina L.; Dawson, Ted M.
CS Department of Neurology, Johns Hopkins University School of Medicine, Baltimore, MD, 21287, USA
SO J. Neurosci. (1998), 18(6), 2040-2055
CODEN: JNRSDS; ISSN: 0270-6474
PB Society for Neuroscience
DT Journal
LA English
AB Neuronal nitric oxide synthase (nNOS) neurons kill adjacent neurons through the action of NMDA-glutamate receptor activation, although they remain relatively resistant to the toxic effects of NMDA and NO. The mol. basis of the resistance of nNOS neurons to toxic insults is unknown. To begin to understand the mol. mechanisms of the resistance of nNOS neurons, we developed a pheochromocytoma-derived cell line (PC12) that is resistant to the toxic effects of NO. We found through serial anal. of |gene| expression (|SAGE|) that manganese superoxide dismutase (MnSOD) is enriched in the NO-resistant PC12 cell-derived line (PC12-R). Antisense MnSOD renders PC12-R cells sensitive to NO toxicity and increases the sensitivity to NO in the parental, NO-sensitive PC12 line (PC12-S). Adenoviral transfer of MnSOD protects PC12-S cells against NO toxicity. We extended these studies to cortical cultures and showed that MnSOD is enriched in nNOS neurons and that antisense MnSOD renders nNOS neurons susceptible to NMDA neurotoxicity, although it

has little effect on the overall susceptibility of cortical neurons to NMDA toxicity. Overexpression of MnSOD provides dramatic protection against NMDA and NO toxicity in cortical cultures, but not against kainate or AMPA neurotoxicity. Furthermore, nNOS neurons from MnSOD-/- mice are markedly sensitive to NMDA toxicity. Adenoviral transfer of MnSOD to MnSOD-/- cultures restores resistance of nNOS neurons to NMDA toxicity. Thus, MnSOD is a major protective protein that appears to be essential for the resistance of nNOS neurons in cortical cultures to NMDA mediated neurotoxicity.

L8 ANSWER 64 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1998:37794 CAPLUS
DN 128:166029
TI Two different primate species express an identical functional MHC class I allele
AU Evans, David T.; Piekarczyk, Marian S.; Cadavid, Luis; Hinshaw, Virginia S.; Watkins, D. I.
CS Wisconsin Regional Primate Research Center, University of Wisconsin, and Department of Pathology + Laboratory Medicine, 1220 Capitol Ct., Madison, WI, 53715, USA
SO Immunogenetics (1998), 47(3), 206-211
CODEN: IMNGBK; ISSN: 0093-7711
PB Springer-Verlag
DT Journal
LA English
AB The products of the highly polymorphic and variable major histocompatibility complex (MHC) class I loci play a crucial role in host defenses against infectious disease. While similar alleles have been found in closely related species, sharing of a functional MHC class I allele between two species has never been reported. Here the authors show that an identical functional MHC class I mol. is present in two different primate species with an approx. divergence time of 0.7 million years. Lymphocytes from the red-crested tamarin (Saguinus geoffroyi) expressed an MHC class I allele (|Sage| -G*01) that was identical in coding sequence to an MHC class I allele (Saoe-G*08) found in the cotton-top tamarin (Saguinus oedipus). Furthermore, influenza virus-specific cytotoxic T lymphocytes (CTLs) generated in the cotton-top tamarin killed lymphocytes expressing the influenza virus nucleoprotein (NP) from the red-crested tamarin. Since the influenza virus NP epitope is bound by Saoe-G*08 in the cotton-top tamarin, it is likely that this mol. is functional in both species. These data provide the first evidence that functional MHC class I mols. can be maintained entirely intact in two sep. species.

L8 ANSWER 65 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:771981 CAPLUS
DN 128:70742
TI Antimutagenic effect of terpenoids from |sage| (Salvia officinalis L.)
AU Simic, Draga; Vukovic-Gacic, Branka; Knezevic-Vukcevic, Jelena; Trninic, Sladana; Jankov, Ratko M.
CS Laboratory of Microbiology, Botanical Institute and Garden "Jevremovac", Faculty of Biology, University of Belgrade, Belgrade, 11000, Yugoslavia SO J. Environ. Pathol., Toxicol. Oncol. (1997), 16(4), 293-301 CODEN: JEPOEC; ISSN: 0731-8898
PB Begell House, Inc.
DT Journal
LA English
AB This is a new Escherichia coli K12 assay system designed to detect bioantimutagens, agents that prevent mutagenesis by modulating |DNA| repair and replication. The test consists of a set of strains aimed at the detection of induced (Test A) and spontaneous (Test B) mutations and at the estn. of the mechanisms of antimutagenic action (Tests B, C, and D). The assay system is intended to screen different exts. of |sage| (Salvia officinalis L.) contg. terpenoids. The results obtained by comparing model bioantimutagens with |sage| exts. indicate that bioantimutagenic agents from cultivated |sage| act as enhancers of error-free recombinational repair. Because cellular |DNA| repair is strongly conserved between prokaryotes and eukaryotes, bioantimutagens from plant exts. could be used in intervention strategies against cancer.

L8 ANSWER 66 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:658943 CAPLUS
DN 127:318182
TI Antioxidants from spices and herbs
AU Nakatani, Nobuji
CS Department Food Nutrition, Faculty Human Life Science, Osaka City University, Japan
SO Furi Rajikaru no Rinsho (1996), 10, 41-47
CODEN: FRRIFI
PB Nihon Igakukan
DT Journal; General Review
LA Japanese
AB A review and discussion with 33 refs., mainly to research by the author and his collaborators. Antioxidants have been used widely throughout the world to prevent or delay oxidn. of fats and oils in a variety of foods. Lipid oxidn., a radical chain reaction of unsatd. fatty acids, causes various kinds of damage not only in foods but also in living organisms. It is a worldwide trend to find effective antioxidants from natural sources. The author and his coworkers have sought new and safe antioxidants, that might be effective in preventing |DNA| , cell and tissue damage which promotes inflammation, cancer and aging, from edible plants, esp. from spices and herbs. New antioxidative compds. have been isolated and their structures were detd. by chem. and spectroscopic means. Examples of new antioxidants are: phenolic diterpenoids from rosemary and |sage| , water-sol. phenolic carboxylic acids derivs. from oregano, biphenyls and flavonoids from thyme, phenolics

substituted by long chain alkyl groups and diarylheptanoids from ginger, phenolic amides from pepper and chili pepper, and others.

L8 ANSWER 67 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:615400 CAPLUS
DN 127:315299
TI A model for p53-induced apoptosis
AU Polyak, Kornelia; Xia, Yong; Zweier, Jay L.; Kinzler, Kenneth W.; Vogelstein, Bert
CS Johns Hopkins Oncology Center, Howard Hughes Medical Institute, Baltimore, MD, 21231, USA
SO Nature (London) (1997), 389(6648), 300-305
CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB The inactivation of the p53 |gene| in a large proportion of human cancers has inspired an intense search for the encoded protein's physiol. and biol. properties. Expression of p53 induces either a stable growth arrest or programmed cell death (apoptosis). In human colorectal cancers, the growth arrest is dependent on the transcriptional induction of the protein p21WAF1/CIP1, but the mechanisms underlying the development of p53-dependent apoptosis are largely unknown. As the most well documented biochem. property of p53 is its ability to activate transcription of |genes| , we examd. in detail the transcripts induced by p53 expression before the onset of apoptosis. Of 7,202 transcripts identified, only 14 (0.19%) were found to be markedly increased in p53-expressing cells compared with control cells. Strikingly, many of these |genes| were predicted to encode proteins that could generate or respond to oxidative stress, including one that is implicated in apoptosis in plant meristems. These observations stimulated addnl. biochem. and pharmacol. expts. suggesting that p53 results in apoptosis through a three-step process: (1) the transcriptional induction of redox-related |genes| ; (2) the formation of reactive oxygen species; and (3) the oxidative degrdn. of mitochondrial components, culminating in cell death.

L8 ANSWER 68 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:606110 CAPLUS
DN 127:288912
TI |SAGE| transcript profiles for p53-dependent growth regulation AU Madden, Stephen L.; Galella, Elizabeth A.; Zhu, Jingshi; Bertelsen, Arthur H.; Beaudry, Gary A.
CS Department of Molecular and Cellular Biology, PharmaGenics, Inc., Allendale, NJ, 07401, USA
SO Oncogene (1997), 15(9), 1079-1085
CODEN: ONCNES; ISSN: 0950-9232
PB Stockton
DT Journal
LA English
AB Serial anal. of |gene| expression (|SAGE|) allows for a quant., representative, and comprehensive profile of |gene| expression. We have utilized |SAGE| technol. to contrast the differential |gene| expression profile in rat embryo fibroblast cells producing temp.-sensitive p53 tumor suppressor protein at permissive or nonpermissive temps. Anal. of .apprx.15 000 |genes| revealed that the expression of 14 |genes| (P<0.001, .ltoreq.0.03% abundance) was dependent on functional p53 protein, whereas the expression of three |genes| was significantly higher in cells producing non-functional p53 protein. Those |genes| whose expression was increased by functional p53 include RAS, U6 snRNA, cyclin G, EGR-1, and several novel |genes| . The expression of actin, tubulin, and HSP70 |genes| was elevated at the nonpermissive temp. for p53 function. Interestingly, the expression of several |genes| was dependent on a non-temp.-sensitive mutant p53 suggesting altered transcription profiles dependent on specific p53 mutant proteins. These results demonstrate the utility of |SAGE| for rapidly and reproducibly evaluating global transcriptional responses within different cell populations.

L8 ANSWER 69 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:278880 CAPLUS
DN 126:247538
TI Method for serial analysis of |gene| expression IN Kinzler, Kenneth W.; Velculescu, Victor E.; Vogelstein, Bert; Zhang, Lin PA Johns Hopkins University School of Medicine, USA
SO Eur. Pat. Appl., 23 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 761822	A2	19970312	EP 1996-306634	19960912
EP 761822	A3	19980805		
R: AT, BE, CH, DE, DK, ES, FR, GR, IT, LI, NL, SE				
US 5695937	A	19971209	US 1995-527154	19950912
US 5866330	A	19990202	US 1995-544861	19951018
PRAI US 1995-527154		19950912		
US 1995-544861		19951018		

AB Serial anal. of |gene| expression (|SAGE|) is described as a method for the rapid quant. and qual. anal. of transcripts. Short defined sequence tags corresponding to a defined position in expressed |genes| (|mRNA|) are isolated and analyzed. The tag is used to identify the corresponding transcript and |gene| from which it is transcribed. By utilizing dimerized tags, termed a ditag, |SAGE| allows elimination of certain types of bias which might occur during cloning and/or amplification and possibly during data evaluation. Concatenation of these short nucleotide sequence tags allows the efficient anal. of transcripts in a serial manner by sequencing multiple tags on a single |DNA| mol, for example, a |DNA| mol. inserted in a vector or in a single clone. Sequencing of over 1000 defined tags in a short period of time

(e.g., hrs.) reveals a |gene| expression pattern characteristics of the function of a cell or tissue. Moreover, |SAGE| is useful as a |gene| discovery tool for the identification in isolation of novel sequence tags corresponding to novel transcripts and |genes| .

L8 ANSWER 70 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:172014 CAPLUS
DN 126:221442
TI Analysis of radiation-induced |gene| expressions by means of serial analysis of |gene| expression (|SAGE|) AU Hara, Takeshi; Namba, Hiroyuki; Yamashita, Shunichi
CS Sch. Med., Nagasaki Univ., Nagasaki, 852, Japan
SO Nagasaki Igakkai Zasshi (1996), 71(Special Iss.), 344-347 CODEN: NAGZAC; ISSN: 0369-3228
PB Nagasaki Igakkai
DT Journal
LA Japanese
AB Serial anal. of |gene| expression (|SAGE|) was useful in evaluation of the |genes| changing expression upon irradn. |SAGE| was applied to WI-38 cells with 10 Gy .gamma.-irradn. |SAGE| was better than subtractive hybridization, differential hybridization and differential display methods.

L8 ANSWER 71 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:94999 CAPLUS
DN 126:153506
TI Characterization of the yeast transcriptome
AU Velculescu, Victor E.; Zhang, Lin; Zhou, Wei; Vogelstein, Jacob; Basrai, Munira A.; Bassett, Douglas E., Jr.; Hieter, Phil; Vogelstein, Bert; Kinzler, Kenneth W.
CS Oncology Center, John Hopkins Univ. School Medicine, Baltimore, MD, 21231, USA
SO Cell (Cambridge, Mass.) (1997), 88(2), 243-251 CODEN: CELLB5; ISSN: 0092-8674
PB Cell Press
DT Journal
LA English
AB We have analyzed the set of |genes| expressed from the yeast genome, herein called the transcriptome, using serial anal. of |gene| expression. Anal. of 60,633 transcripts revealed 4,665 |genes| , with expression levels ranging from 0.3 to over 200 transcripts per cell. Of these |genes| , 1981 had known functions, while 2684 were previously uncharacterized. The integration of positional information with |gene| expression data allowed for the generation of chromosomal expression maps identifying phys. regions of transcriptional activity and identified |genes| that had not been predicted by sequence information alone. These studies provide insight into global patterns of |gene| expression in yeast and demonstrate the feasibility of genome-wide expression studies in eukaryotes.

L8 ANSWER 72 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1997:55752 CAPLUS
DN 126:221377
TI Mutational analysis of the nor |gene| cluster which encodes nitric oxide reductase from Paracoccus denitrificans
AU De Boer, Anthonius P. N.; Van der Oost, John; Reijnders, Willem N. M.; Westerhoff, Hans V.; Stouthamer, Adriaan H.; Van Spanning, Rob J. M. CS Faculty Biology, Vrije Universiteit Amsterdam, Amsterdam, 1081 HV, Neth. SO Eur. J. Biochem. (1996), 242(3), 592-600
CODEN: EJBCAI; ISSN: 0014-2956
PB Springer
DT Journal
LA English
AB The |genes| that encode the bc-type NO reductase from P. denitrificans were identified. They are part of a cluster of 6 |genes| (norCBQDEF) and are found near the |gene| cluster that encodes the cd1-type nitrite reductase. |Genes| norC and norB encode the cytochrome-c-contg. subunit II and cytochrome-b-contg. subunit I of NO reductase, resp. |Gene| norQ encodes a protein with an ATP-binding motif and has high similarity to NirQ from Pseudomonas stutzeri and Pseudomonas aeruginosa, and CbbQ from Pseudomonas hydrogenothermophila. |Gene| norE encodes a protein with 5 putative transmembrane a-helixes and has similarity to CoxIII, the 3rd subunit of the aa3-type cytochrome-c oxidases. |Gene| |norF| encodes a small protein with 2 putative transmembrane .alpha.-helixes. Mutagenesis of norC, norB, norQ and norD resulted in cells unable to grow anaerobically. Nitrite reductase and NO reductase (with succinate or ascorbate as substrates) and nitrous oxide reductase (with succinate as substrate) activities were not detected in these mutant strains. Nitrite extrusion was detected in the medium, indicating that nitrate reductase was active. The norQ and norD mutant strains retained about 16% and 23% of the wild-type level of NorC, resp. The norE and |norF| mutant strains had specific growth rates and NorC contents similar to those of the wild-type strain, but had reduced NOR and NIR activities, indicating that their |gene| products are involved in regulation of enzyme activity. Mutant strains contg. the norCBQDEF region on the broad-host-range vector pEG400 were able to grow anaerobically, although at a lower specific growth rate and with lower NOR activity compared with the wild-type strain.

L8 ANSWER 73 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1996:562102 CAPLUS
DN 125:245076
TI MHC class I-processed pseudogenes in New World primates provide evidence for rapid turnover of MHC class I |genes|
AU Cadavid, Luis F.; Hughes, Austin L.; Watkins, David I. CS Wisconsin Regional Primate Research Center, University Wisconsin, Madison, WI, 53715, USA
SO J. Immunol. (1996), 157(6), 2403-2409
CODEN: JOIMA3; ISSN: 0022-1767
DT Journal

LA English
AB The MHC class I |genes| of the New World primate, the cotton-top tamarin (Saguinus oedipus), are an exception to the high polymorphism and variability displayed by this multigene family. The authors report the isolation of the first two processed pseudogenes from the MHC region in primates. These two MHC class I-processed pseudogenes (MHC-PS1 and -PS2) were found in several species of New World primates, suggesting a possible explanation for the cotton-top tamarin's limited MHC class I diversity. The pattern of synonymous and nonsynonymous substitutions in PS1 suggests that the |gene| that gave rise to this processed pseudogene was once subject to selection for variability in the peptide binding region and might, therefore, have been functional. Addnl., PS1 is not closely related to the expressed cotton-top tamarin's MHC class I |gene| , but does show some similarity to So-N1, a tamarin pseudogene from which no transcript has been found. Thus, PS1 may represent a remnant of a once active MHC class I |gene| that is no longer functional in the cotton-top tamarin. The MHC class I loci in primates, therefore, appear to be evolving by a continual process of duplication and inactivation. This process seems to be exaggerated in New World primates and may in part be responsible for the cotton-top tamarin's limited MHC class I diversity.

L8 ANSWER 74 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1996:301828 CAPLUS
DN 124:334146
TI Serial analysis of |gene| expression: ESTs get smaller AU Adams, Mark D.
CS Institute Genomic Research, Rockville, MD, 20850, USA SO BioEssays (1996), 18(4), 261-262
CODEN: BIOEEJ; ISSN: 0265-9247
DT Journal
LA English
AB Measuring |gene| expression on a global scale has been one of the vexing problems of cell biol. Velculescu et al. recently proposed a system for identifying |gene| expression levels based on very short sequence tags - about nine base pairs - located at a specific site within a |gene| transcript. By coupling the strategy to current automated sequencing machines and the large expressed sequence tag databases, it should be possible to follow changes in |gene| expression for large nos. of |genes| economically and accurately.

L8 ANSWER 75 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1995:883831 CAPLUS
DN 124:22666
TI Serial analysis of |gene| expression
AU Velculescu, Victor E.; Zhang, Lin; Vogelstein, Bert; Kinzler, Kenneth W. CS Oncology Center, Johns Hopkins University, Baltimore, MD, 21231, USA SO Science (Washington, D. C.) (1995), 270(5235), 484-7
CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
AB The characteristics of an organism are detd. by the |genes| expressed within it. A method was developed, called serial anal. of |gene| expression (|SAGE|), that allows the quant. and simultaneous anal. of a large no. of transcripts. To demonstrate this strategy, short diagnostic sequence tags were isolated from pancreas, concatenated, and cloned. Manual sequencing of 1000 tags revealed a |gene| expression pattern characteristic of pancreatic function. New pancreatic transcripts corresponding to novel tags were identified. |SAGE| should provide a broadly applicable means for the quant. cataloging and comparison of expressed |genes| in a variety of normal, developmental, and disease states.

L8 ANSWER 76 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1995:616287 CAPLUS
DN 123:134496
TI Distribution of the p53 pseudogene among mouse species and subspecies AU Tanooka, H.; Ootsuyama, A.; Shiroishi, T.; Moriwaki, K. CS Radiobiology Division, National Cancer Center Research Institute, Tokyo, 104, Japan
SO Mamm. Genome (1995), 6(5), 360-2
CODEN: MAMGEC; ISSN: 0938-8990
DT Journal
LA English
AB Pseudogenes may provide a useful marker for mol. taxonomy, since the rate of nucleotide substitutions for pseudogenes is much higher than that for functional |genes| (Nei 1987). The present article gives evidence that the p53 pseudogene is useful for classification of mouse subspecies. In the present study, we examd. |DNA| of various wild mic captured at different localities for p53 pseudogene variation, to gain information on the origin and evolution of mice. We found that the p53 pseudogene was present in eight samples and absent in 14 samples. Only one p53 pseudogene band was found per mouse, unlike the multiple p53 pseudogenes in the rat (Weghorst et at. 1993). The polymorphism of the p53 pseudogenes among the surveyed Mus species and Mus musculus subspecies in relation to the phylogenic tree of the mouse (|Sage| 1981; Bonhomme et at. 1984; Moriwaki et al. 1986, 1990). M. musculus subspecies in northern China is still in argument for its classification, but here it is tentatively classified as M. musculus. The majority of the surveyed group - M. spretus in Spain, M. m. bactrianus in Iran and Pakistan, M. m. musculus in Bulgaria, northern China, Denmark, Korea, and Poland, and M. m. molossinus in Japan - do not possess the p53 pseudogene. In addn., the p53 pseudogene was absent in M. caroli; M. spicilegus in Bulgaria possesses type I p53 pseudogene, Psip53.1. On the other hand, M. m. domesticus in Bulgaria and Canada, M. m. brevirostris in France, and M. m. castaneus in Malaysia and Guiling of southern China share type II p53 pseudogene, Psip53.2, whereas M. m. castaneus in Sumatra of Indonesia and Taiwan, sepd. by the sea from the continent, possesses type III p53 pseudogene,

Psip53.2.1, which is thought to have been derived from type II p53 pseudogene. Mutational variations in the p53 pseudogene are in accord with the classification of the mouse proposed by Moriwaki and assocs. (1986, 1990) on the basis of various mol. markers; wild mice widely distributed in Asia and Europe, M. m. musculus, do not possess the p53 pseudogene. These groups include wild mice in northern China, Korea, and Japan. all of which have musculus-specific mitochondria |DNA| (Yonekawa et at. 1986). In accord with the finding that wild mice in southern China have castaneus-specific mitochondria |DNA| (Yonekawa et al. 1986), these mice do possess the p53 pseudogene of type II. Bulgaria appeared to be a hybrid zone from the p53 pseudogene variety, as has been known (Boursot et al. 1984). Type 11 was also found in lab. mice of the Swiss albino-derived ICR strain and cultured cells of BALB/3T3, which have been known to be of the domesticus origin (Yonekawa et at. 1982). Of the three types of p53 pseudogenes, Psip53.2.1 is very likely to have evolved from Psip53.2 as mentioned above. The two types of Psip53, Psip53.1 and Psip53.2, are possessed by a minority of the surveyed wild mice, indicating that integration of the p53 pseudogene occurred once or twice during evolution of the ancestral mouse, probably as a form of the processed p53 pseudogene.

L8 ANSWER 77 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1995:319364 CAPLUS
DN 122:102539
TI Inhibition of endothelial cell proliferation by SPARC is mediated through a Ca2+-binding EF-hand sequence
AU Sage, E. Helene; Bassuk, James A.; Yost, Jeffrey C.; Folkman, M. Judah; Lane, Timothy F.
CS Sch. Med., Univ. Washington, Seattle, WA, 98195, USA
SO J. Cell. Biochem. (1995), 57(1), 127-40
CODEN: JCEBD5; ISSN: 0730-2312
DT Journal
LA English
AB SPARC (secreted protein, acidic and rich in cysteine, also known as osteonectin and BM-40) is a metal-binding glycoprotein secreted by a variety of cultured cells and characteristic of tissues undergoing morphogenesis, remodeling, and repair. Recently it has been shown that SPARC inhibits the progression of the endothelial cell cycle in mid-G1, and that a synthetic peptide (amino acids 54-73 of secreted murine SPARC, peptide 2.1) from a cationic, disulfide-bonded region was in part responsible for the growth-suppressing activity (Funk, S. E.; |Sage| , E. H., 1991). Moreover, SPARC was shown to interact directly with bovine aortic endothelial (BAE) cells through a C-terminal EF-hand sequence comprising a high-affinity Ca2+-binding site of SPARC and represented by a synthetic peptide (amino acids 254-273) termed 4.2 (Yost, J. C.; |Sage| , E. H., 1993). In this study the authors show that peptide 4.2 is a more potent inhibitor of |DNA| synthesis that acts cooperatively with peptide 2.1 to diminish the incorporation of [3H]thymidine by both BAE and bovine capillary endothelial (BCE) cells. At concns. of 0.019-0.26 mM peptide 4.2, thymidine incorporation by BAE cells was decreased incrementally, relative to control values, from approx. 100 to 10%. Although somewhat less responsive, BCE cells exhibited a dose-responsive decrement in thymidine incorporation, with a maximal inhibition of 55% at 0.39 mM. The inhibitory effect of peptide 4.2 was essentially independent of heparin and basic fibroblast growth factor and was blocked by anti-SPARC peptide 4.2 IgG, but not by antibodies specific for other domains of SPARC. To identify residues that were necessary for inhibition of |DNA| synthesis, the authors introduced single amino acid substitutions into synthetic peptide 4.2 and tested their activities and cell-surface binding characteristics on endothelial cells. Two peptides displayed null to diminished effects in the bioassays that were concn.-dependent: peptide 4.2 K, contg. an Asp258 .fwdarw. Lys substitution, and peptide 4.2 AA, in which the two disulfide-bonded Cys (positions 255 and 271) were changed to Ala residues. Peptide 4.2 K, which failed to fulfill the EF-hand consensus formula, exhibited an anomalous fluorescence emission spectrum, in comparison with the wild-type 4.2 sequence, that was indicative of a compromised affinity for Ca2+. Moreover, ablation of the disulfide bond in peptide 4.2 AA potentially destabilized the Ca2+-binding loop structure, as assessed by fluorescence spectroscopy, such that the peptide competed poorly for the binding of [125I]-peptide 4.2 to BAE cells. The authors conclude that both the Ca2+-coordinating Asp at position 258 and the conformation of peptide 4.2 are necessary for the inhibition of |DNA| synthesis by SPARC in cultured endothelial cells.

L8 ANSWER 78 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1995:195838 CAPLUS
DN 122:209508
TI Molecular systematics of the Nepetoideae (family Labiatae): phylogenetic implications from rbcL |gene| sequences
AU Kaufmann, Martina; Wink, Michael
CS Inst. Pharmazeutische Biol., Univ. Heidelberg, Heidelberg, D-69120, Germany
SO Z. Naturforsch., C: Biosci. (1994), 49(9/10), 635-45 CODEN: ZNCBDA; ISSN: 0341-0382
DT Journal
LA English
AB Total |DNA| was extd. from 41 species (20 genera) of the subfamily Nepetoideae (family Labiatae). Using rbcL-specific primers, the rbcL |gene| was amplified by PCR and sequenced directly. RbcL sequences were evaluated with character state (max. parsimony; PAUP) and distance methods (neighbor-joining: MEGA). In agreement with classical systematics all taxa studied cluster within the Nepetoideae and are clearly distinguished from members of the subfamily

Lamioideae. A no. of distinctive clades are apparent within the Nepetoideae: I - Collinsonia, II - Lavandula, III - Agastache, Glechoma, IV - Satureja, Hyssopus, Dracocephalum, V - Nepeta, VI - Hormium, VII - Prunella, VIII - Melissa, Ocimum, IX - Monarda, Mentha, X - Origanum, Thymus, XI - Salvia, XII - Rosmarinus, and XIII - Perovskia. At least 5 main branches representing the clades I, II, III-VII, VIII, and IX-XIII, resp., can be distinguished within the Nepetoideae studied. They might be considered representing the tribes (according to P. D. Cantino et al., 1992) Elsholtzieae (I), Lavanduleae (II), and Mentheae (III-XIII). The tribe Mentheae needs to be subdivided into at least 3 main groups (clades III-VII, VIII, and IX-XIII). Majorana hortensis which is often classified as Origanum hortensis does not cluster with Origanum and deserves a generic status of its own.

L8 ANSWER 79 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1994:572831 CAPLUS
DN 121:172831
TI Effects of ginseng and Salvia miltiorrhiza extracts on the mutagenicity of MNNG in Drosophila
AU Choi, Yung-Hyun; Chung, Hae-Young; Yoo, Mi-Ae; Lee, Won-Ho CS Dept. Biology, Pusan National Univ., Pusan, 609-735, S. Korea SO Yakhak Hoechi (1994), 38(3), 332-7
CODEN: YAHOA3; ISSN: 0513-4234
DT Journal
LA Korean
AB Using geminal and somatic cell mutation assaying systems of Drosophila melanogaster, effects of Ginseng and Salvia miltiorrhiza exts. on the in vivo mutagenicity induced by MNNG were investigated. For these purposes, the attached-X method and the mwh/flr spot test system which are an X-linked lethal mutation and a somatic chromosome mutations during the spermatogenesis, MNNG showed more actions in the sperm and spermatid stages, in which Ginseng and Salvia miltiorrhiza ext. had remarkable inhibitory effects than other stages. Ginseng and Salvia miltiorrhiza exts. reduced the mutagenicity by MNNG in the mwh/flr system, which reveal that they can inhibit |gene| mutation, deletion and mitotic chromosomal recombination. These results seem to suggest that Ginseng and Salvia miltiorrhiza exts. may exert their inhibitory effects in vivo mutagenic and/or carcinogenic properties of |DNA| -damaging agents.

L8 ANSWER 80 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1994:571499 CAPLUS
DN 121:171499
TI A PCR-based assay for wheat soilborne mosaic virus in hard red winter wheat
AU Pennington, R. E.; Sherwood, J. L.; Hunger, R. M. CS Dep. Plant Pathol., Oklahoma State Univ., Stillwater, OK, 74078, USA SO Plant Dis. (1993), 77(12), 1202-5
CODEN: PLDIDE; ISSN: 0191-2917
DT Journal
LA English
AB A reverse transcription (RT)-polymerase chain reaction (PCR)-based assay that allows individual detection of |RNA1| and |RNA2| of wheat soilborne mosaic virus (WSBMV) was developed and utilized in conjunction with ELISA to detect WSBMV in Triticum aestivum. Resistant cultivars Newton and Hawk and susceptible cultivars Vona and |Sage| were planted 30 Sept. 1991 in a field with a history of severe wheat soilborne mosaic. In ELISA, WSBMV was detected only rarely in root samples from either susceptible or resistant cultivars taken on 16 Oct. or 2 Nov. but in nearly all root samples taken on or after 4 Dec. |RNA2| was detected in all ELISA-pos. root samples and in most ELISA-neg. root samples from either susceptible or resistant cultivars. Thus, |RNA2| could be found in root samples of susceptible or resistant cultivars up to 7 wk before virus could be detected by ELISA. |RNA1| was detected in most samples in which |RNA2| was detected but was detected only rarely in samples in which |RNA2| was not detected. In ELISA and/or RT-PCR, WSBMV was detected in most foliar samples from susceptible cultivars taken on or after 4 Dec. In ELISA and/or RT-PCR of foliar samples from resistant cultivars, however, detection of WSBMV was limited until the 1 Mar. sampling. These results support the use of ELISA for evaluating cultivars for resistance to WSBMV and support the hypothesis that resistance is expressed as an inhibition of virus movement. The results do not support the possibility that resistance is expressed differentially against the two WSBMV |RNAs| .

L8 ANSWER 81 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1994:499753 CAPLUS
DN 121:99753
TI Inhibition of collagen hydroxylation by lithospermic acid magnesium salt, a novel compound isolated from Salviae miltiorrhizae Radix AU Shigematsu, Takeshi; Tajima, Shingo; Nishikawa, Takeji; Murad, Saood; Pinnell, Sheldon R.; Nishioka, Itsuo
CS Research Laboratories, Pias Corporation, Osaka, Japan SO Biochim. Biophys. Acta (1994), 1200(1), 79-83
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
AB The authors have screened several Chinese medicinal herbs for the presence of antifibrotic agents. An aq. ext. of Salviae miltiorrhizae Radix was found to inhibit collagen secretion by human skin fibroblasts without affecting |DNA| or non-collagen protein synthesis. The authors have subsequently purified the material exhibiting the inhibitory activity and identified it as magnesium lithospermate. From its chem. structure, this compd. was predicted to be an inhibitor of the post-translational modifying enzymes prolyl and lysyl hydroxylases in collagen biosynthesis. Accordingly, it decreased the extent of prolyl and lysyl hydroxylations in collagen by approx.

50%. Added to cell exts., it inhibited both prolyl and lysyl hydroxylase activities, but only lysyl hydroxylase activity when added to intact cells. Oral administration of this compd. to mice led to a significant redn. of prolyl hydroxylation in newly-synthesized skin collagen. This naturally-occurring compd. thus offers a potential means for treating fibrotic diseases, such as systemic scleroderma and keloid.

L8 ANSWER 82 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1994:24765 CAPLUS
DN 120:24765
TI Evidence for linkage of the apolipoprotein A-II locus to plasma apolipoprotein A-II and free fatty acid levels in mice and humans AU Warden, Craig H.; Daluiski, Aaron; Bu, Xiangdong; Purcell-Huynh, Deborah A.; De Meester, Cynthia; Shieh, Bie Huoy; Puppione, Donald L.; Gray, Richard M.; Reaven, Gerald M.; et al.
CS Dep. Med., Univ. California, Los Angeles, CA, 90024, USA SO Proc. Natl. Acad. Sci. U. S. A. (1993), 90(22), 10886-90 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Although it has been hypothesized that the synteny between mouse and human |genes| provides an approach to the localization of |genes| that det. quant. traits in humans, this has yet to be demonstrated. The authors tested this approach with two quant. traits, plasma apolipoprotein A-II (apoAII) and free fatty acid (FFA) levels. ApoAII is the second most abundant protein of high d. lipoprotein particles, but its function remains largely unknown. The authors now show that, in a backcross between strains Mus spretus and C57BL/6J, apoAII levels correlate with plasma FFA concns. on both chow and high-fat diets and that apoAII levels are linked to the apoAII |gene| . To test whether variations of the apoAII |gene| influence plasma lipid metab. in humans, the authors studied 306 individuals in 25 families enriched for coronary artery disease. The segregation of the apoAII |gene| was followed by using an informative simple sequence repeat in the second intron of the |gene| and two nearby genetic markers. Robust sib-pair linkage anal. was performed on members of these families using the |SAGE| linkage programs. The results suggest linkage between the human apoAII |gene| and a |gene| controlling plasma apoAII levels. Plasma apoAII levels were also significantly correlated with plasma FFA levels. Moreover, the apoAII |gene| exhibited linkage with a |gene| controlling FFA levels. Evidence for nonrandom segregation was seen with markers as far as 6-12 centimorgans from the apoAII structural locus. These data provide evidence, in two species, that the apoAII |gene| is linked to a |gene| that controls plasma apoAII levels and that apoAII influences, by an unknown mechanism, plasma FFA levels. The results illustrate the utility of animal studies for anal. of complex traits.

L8 ANSWER 83 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1993:96763 CAPLUS
DN 118:96763
TI Inhibition of protein synthesis in cell-free system by single chain ribosome-inactivating proteins
AU Wang, Runhua; Zheng, Suo; Chen, Xing; Shen, Beifen
CS Inst. Basic Med. Sci., Acad. Mil. Med. Sci., Beijing, 100850, Peop. Rep. China
SO Shengwu Huaxue Zazhi (1992), 8(4), 395-9
CODEN: SHZAE4; ISSN: 1000-8543
DT Journal
LA Chinese
AB Ribosome-inactivating proteins (RIPs), which are widespread throughout the plant kingdom, are a specific type of |RNA| N-glycosidase which inactivates ribosome 60 S subunits. Here, 13 different toxic and nontoxic single-chain RIPs were isolated and purified for comparison of their inhibitory activities with respect to protein synthesis in rabbit reticulocyte lysate and their cytotoxicities to intact cells.

L8 ANSWER 84 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1991:519803 CAPLUS
DN 115:119803
TI Studies on the genotoxic properties of essential oils with Bacillus subtilis rec-assay and Salmonella/microsome reversion assay AU Zani, F.; Massimo, G.; Benvenuti, S.; Bianchi, A.; Albasini, A.; Melegari, M.; Vampa, G.; Bellotti, A.; Mazza, P.
CS Fac. Farm., Univ. Parma, Parma, I-43100, Italy
SO Planta Med. (1991), 57(3), 237-41
CODEN: PLMEAA; ISSN: 0032-0943
DT Journal
LA English
AB Genotoxic properties of essential oils from Anthemis nobilis, Artemisia dracunculus, Salvia officinalis, S. sclarea, Satureja hortensis, S. montana, Thymus capitatus, T. citriodorus, T. vulgaris, and Citrus bergamia Risso, were studied with B. subtilis rec-assay and Salmonella/microsome reversion assay. The essential oil of Artemisia dracunculus "Piemontese" was active in the rec-assay but not in the Salmonella test. |DNA| -damaging activity was demonstrated to be due to the estragol component of the oil. Advantages of the combined use of these two short-term microbial assays in genotoxic studies are discussed.

L8 ANSWER 85 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1991:182879 CAPLUS
DN 114:182879
TI Differential expression of extracellular proteins is correlated with angiogenesis in vitro
AU Iruela-Arispe, Maria Luisa; Hasselaar, Paula; Sage, Helene CS Dep. Biol. Struct., Univ. Washington, Seattle, WA, 98195, USA SO Lab. Invest. (1991), 64(2), 174-86
CODEN: LAINAW; ISSN: 0023-6837
DT Journal
LA English
AB Strains of bovine aortic endothelial cells, grown on plastic under conventional culture conditions and

in the absence of growth factor supplementation, exhibited a sprouting phenotype and a predisposition toward the formation of cords and tubular structures. Endothelial cells at different stages of tube formation were examd. Anal. of metabolically labeled proteins showed that the synthesis of type I collagen was initiated in sprouting cells and during the formation of tubular structures. SPARC (secreted protein, acidic and rich in cysteine), a Ca2+-binding protein assocd. with cellular shape change and morphogenetic processes (|Sage| H; et al., 1989), was upregulated during spontaneous tube formation. Levels of |mRNA| for type I collagen and SPARC corroborated the stage-specific increases obsd. for these proteins. Differential levels of transcription were apparent in multilayered cells directly involved in tube formation, in comparison with cells comprising either the tubes or the confluent monolayers at a distance from the tubes. Anal. of |DNA| synthesis indicated that multilayered, sprouting cells in the proximity of the endothelial tubes were actively proliferating, whereas cells that had been incorporated into tubes showed low levels of |DNA| synthesis. Immunolabeling studies revealed a dense accumulation of SPARC and type I collagen in the cytoplasm of cells that were situated near the growing tubes. Two other secreted proteins, type III collagen and thrombospondin, were expressed constitutively by subconfluent cultures and were increased in those cells contributing to tube formation. Evidently, type I collagen and SPARC are specifically related to the angiogenesis-like phenomenon displayed by bovine aortic endothelial cells in vitro. Type I collagen might facilitate the active migration of endothelial cells, or the stabilization of the resulting tubes, with SPARC directing the re-organization and dynamic assembly of the tubular network.

L8 ANSWER 86 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1990:527691 CAPLUS
DN 113:127691
TI Overexpression of phytochrome in transgenic plants
IN Hershey, Howard P.; Keller, Janis M.
PA du Pont de Nemours, E. I., and Co., USA
SO Eur. Pat. Appl., 42 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 354687	A1	19900214	EP 1989-307658	19890727
EP 354687	B1	19940928		
R: ES, GR				
US 5268526	A	19931207	US 1988-284422	19881214
WO 9001261	A1	19900222	WO 1989-US3178	19890727
W: AU, HU, JP				
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
AU 8939734	A1	19900305	AU 1989-39734	19890727
EP 430972	A1	19910612	EP 1989-908631	19890727
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
JP 04500002	T2	19920109	JP 1989-508139	19890727

PRAI US 1988-226344 19880729
US 1988-284422 19881214
WO 1989-US3178 19890727

AB Transgenic plants which overexpress phytochrome relative to wild-type plants both in the light and the dark are produced. These plants display reduced apical dominance, semidwarfism, increased shade tolerance, and/or dark green color. Plasmid pCV5B3, contg. a continuous coding region for Avena phytochrome, was constructed from plasmids contg. fragments of the phytochrome |gene| . This |gene| was removed from pCV5B3 and fused with the cauliflower mosaic virus 35S promoter to prep. plasmid pCV34phyt which was transferred to Agrobacterium tumefaciens by triparental mating. The chimeric |gene| was introduced into tobacco by A. tumefaciens infection of leaf disks followed by regeneration of tobacco plants. Transgenic plants producing increased phytochrome (immunochem. anal.) showed increased green pigmentation, increased tillering, reduced apical dominance, and reduced internodal distance. These plants flowered at the same time as normal plants and had comparable seed yield per inflorescence. In dark-grown transgenic seedlings, there was 50% more phytochrome activity than in controls; in light-grown seedlings, there was 10-fold more activity.

L8 ANSWER 87 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1990:211998 CAPLUS
DN 112:211998
TI Transgenic tobacco plants with modified physiology and morphology, due to expression of agrobacterium or plasmid |genes| IN Spena, Angelo; Schmuelling, Thomas; Salamini, Francesco; Schell, Joseph S. PA Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V., Fed. Rep. Ger.
SO Eur. Pat. Appl., 21 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 334383	A2	19890927	EP 1989-105307	19890323
EP 334383	A3	19900131		
R: ES, GR				
DE 3810286	A1	19891012	DE 1988-3810286	19880325
DE 3810286	C2	19900705		
WO 8909262	A2	19891005	WO 1989-EP319	19890323
WO 8909262	A3	19891228		
W: AU, BR, DK, FI, HU, US				
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
AU 8933589	A1	19891016	AU 1989-33589	19890323
AU 633484	B2	19930204		

ZA 8902206 A 19891129 ZA 1989-2206 19890323 EP 362349 A1 19900411 EP 1989-904046 19890323 EP 362349 B1 19951227
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE
HU 52159 A2 19900628 HU 1989-2098 19890323 BR 8906478 A 19901127 BR 1989-6478 19890323 AT 132188 E 19960115 AT 1989-904046 19890323 ES 2083391 T3 19960416 ES 1989-904046 19890323 DK 8905943 A 19891124 DK 1989-5943 19891124 PRAI DE 1988-3810286 19880325
WO 1989-EP319 19890323
AB Plasmids encoding all possible combinations of the rol |genes| of the Ri-plasmid of Agrobacterium tumefaciens under the control of inducible or constitutive promoters are introduced into tobacco tissue cultures and transgenic plants regenerated. The regenerated plants have modified physiol., morphol., and hormone metab. and these plants constitute novel germplasm with many uses in plant breeding. Plants carrying all three |genes| showed typical hairy-root syndrome. Plants contg. only two of these |genes| showed alterations including altered leaf shape, enlarged or smaller stigma and flowers, altered flowering period etc. These traits appear to be stably inherited and co-segregate with kanamycin resistance.

L8 ANSWER 88 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1989:437033 CAPLUS
DN 111:37033
TI Tissue and age specific expression of the myc proto-oncogene family throughout the life span of the C57BL/6J mouse strain AU Semsei, Imre; Ma, Shuyi; Cutler, Richard G.
CS Gerontol. Res. Cent., Natl. Inst. Aging, Baltimore, MD, 21224, USA SO Oncogene (1989), 4(4), 465-71
CODEN: ONCNES; ISSN: 0950-9232
DT Journal
LA English
AB The expression of the proto-oncogene myc family in terms of steady-state |mRNA| levels was detd. in 7 different normal non-cancerous tissues throughout the life span (7 different ages) of the C57BL/6J male mouse strain. Expression of the c-myc oncogene was highest in prenatal and newborn ages and then decreased to its lowest levels at .apprx.6 mo of age. With further increase of age, a progressive pattern of increase in expression of c-myc was found in brain, liver, skin, and small intestine. For kidney, spleen and heart, little or no significant change was evident. Significant differential expression of c-myc was found in most tissues in animals of the same |sage| , with highest expression consistently being found in spleen and liver at all ages. For the N-myc and L-myc oncogenes, expression was also highest in prenatal and newborn tissue as compared to the 6-mo young adult, but little or no further change was found at older ages. Substantial tissue-dependent differences in expression were also found, and no expression at all was detected at any age for N-myc in liver and for L-myc in heart, small intestine and liver. Apparently, the expression of the proto-oncogenes c-, L-, and N-myc is dependent not only on tissue and embryonic development, but also on age past the young adult stage of life span. The age-dependent increase in expression of c-myc oncogene found in normal-appearing non-cancerous tissues is of particular interest as possibly reflecting tissue alterations related to both the aging process and the age-dependent increase in cancer incidence.

L8 ANSWER 89 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1988:402112 CAPLUS
DN 109:2112
TI Evaluation of chemical genotoxicity by a series of short-term tests AU Hachiya, Noriyuki
CS Sch. Med., Akita Univ., Akita, Japan
SO Akita Igaku (1987), 14(2), 269-92
CODEN: AKIGDV; ISSN: 0386-6106
DT Journal
LA Japanese
AB To evaluate chem. genotoxicity, 82 substances were subjected to a battery of short-term assays. Tested materials include 64 chems. used in plastic industries, and 16 natural products which are currently used as food additives in Japan. The ability to induce micronuclei in mouse bone marrow was examd. for 26 materials.

L8 ANSWER 90 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1988:183777 CAPLUS
DN 108:183777
TI Isoelectric focusing patterns of kernel isozymes from 80 North American winter wheat cultivars
AU Cox, T. S.; Murphy, J. P.; Harrell, L. G.
CS Dep. Agron., Kansas State Univ., Manhattan, KS, 66506, USA SO Can. J. Plant Sci. (1988), 68(1), 65-72
CODEN: CPLSAY; ISSN: 0008-4220
DT Journal
LA English
AB The cataloging of wheat (Triticum aestivum) cultivar isoenzyme patterns, a routine exercise, provides useful data for genetic and breeding studies. Isoenzymes of 5 kernel enzyme systems (.beta.-amylase, esterases, malate dehydrogenase, superoxide dismutase, and glucose phosphate isomerase) were sepd. by isoelec. focusing (IEF) for 80 North American winter wheat cultivars. No variation in malate dehydrogenase, superoxide dismutase, or glucose phosphate isomerase IEF patterns was detected. There were 3 groups of hard red winter wheat cultivars with esterase patterns that differed from the pattern common to all others; Arkan and |Sage| ; Siouxland, Colt, and Pioneer 2157; and Sandy. Esterase IEF, in contrast to gliadin electrophoresis in other studies, distinguished |Sage| from Eagle and Larned. Four soft red winter cultivars (Compton and Adena; Florida 302; Roland) and six groups contg. a total of 8 hard red winter cultivars (RHS812; RHS830; Norstar; Plainsman V; TAM 105, TAM 107, and Rose; and TAM 101) had variant .beta.-amylase patterns. Some of the esterase and .beta.-amylase variants, produced by |genes| on chromosomes 3A, 3D,

4D, 5A, and possibly others, may be useful in linkage studies.

L8 ANSWER 91 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1984:609264 CAPLUS
DN 101:209264
TI Primary mutagenicity screening of food additives currently used in Japan AU Ishidate, M., Jr.; Sofuni, T.; Yoshikawa, K.; Hayashi, M.; Nohmi, T.; Sawada, M.; Matsuoka, A.
CS Biol. Saf. Res. Cent., Natl. Inst. Hyg. Sci., Tokyo, 158, Japan SO Food Chem. Toxicol. (1984), 22(8), 623-36
CODEN: FCTOD7; ISSN: 0278-6915
DT Journal
LA English
AB Salmonella/Microsome tests (Ames tests) and chromosomal aberration tests in vitro using a Chinese hamster fibroblast cell line were carried out on 190 synthetic food additives and 52 food additives derived from natural sources, all of which are currently used in Japan. Fourteen out of 200 tested in the Ames assay showed pos. effects and 54 out of 242 were pos. in the chromosome test. Three additives (erythorbic acid [89-65-6], ClO2, and beet red) were pos. only in the Ames test, although their mutagenic potentials were relatively weak, while 43 additives were pos. only in the chromosome test. Eleven additives, Ca(OCl)2, cinnamic aldehyde [104-55-2], L-cysteine.HCl [52-89-1], Food Green No. 3 (Fast Green FCF) [2353-45-9], H2O2, KBrO3, NaClO2, NaOCl, NaNO2, cacao pigment, and caramel, were pos. in both the Ames test and the chromosome test. The usefulness of such primary screening tests combining 2 different genetic end-points, |gene| mutation and chromosomal aberration, and some correlation between mutagenicity and carcinogenicity of food additives are discussed.

L8 ANSWER 92 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1984:400230 CAPLUS
DN 101:230
TI Chemical and pharmacological studies of Salvia tomentosa AU Ulubelen, Ayhan; Miski, Mahmut; Johansson, Candan
CS Eczacilik Fak., IU, Istanbul, Turk.
SO Doga, Seri C (1984), 8(1), 109-15
CODEN: DSTIDB; ISSN: 0254-2331
DT Journal
LA Turkish
AB Extn. of S. tomentosa with petroleum ether, benzene, CCl4, and alc. followed by polyamide and silica gel chromatog., permitted the isolation of several pharmacol. active compds. Antiochic acid [77091-10-2] was cytotoxic to L cells in culture; 6-hydroxyluteolin-7-glucoside [54300-65-1] inhibited |DNA| formation in these cells. Cirsimaritin [6601-62-3] and dehydroabietic acid [1740-19-8] were bactericidal to may Gram-pos. and -neg. bacteria.

L8 ANSWER 93 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1984:20935 CAPLUS
DN 100:20935
TI Mitochondrial |DNA| evolution in mice
AU Ferris, Stephen D.; Sage, Richard D.; Prager, Ellen M.; Ritte, Uzi; Wilson, Allan C.
CS Dep. Biochem., Univ. California, Berkeley, CA, 94720, USA SO Genetics (1983), 105(3), 681-721
CODEN: GENTAE; ISSN: 0016-6731
DT Journal
LA English
AB This study extends knowledge of mitochondria |DNA| (mtDNA) diversity in mice to include animals belonging to 8 species in the subgenus Mus. Highly purified mtDNA from each was subjected to high-resoln. restriction mapping with respect to the known sequence of 1 mouse mtDNA. Variation attributed to base substitutions was encountered at .apprx.2/3 of the cleavage sites examd., and a length mutation was located in or near the displacement loop. The variability of different functional regions in this genome was as follows, from least to most: rRNA, tRNA, known proteins, displacement loop, and unidentified reading frames. Phylogenetic anal. confirmed the utility of the J. T. Marshall and R. D. |Sage| (1981) revision of mouse classification, according to which there are .gtoreq.4 species of commensal mice and 3 species of aboriginal mice in the complex that was formerly considered to be 1 species. The level of mtDNA variation among wild representative of Mus domesticus is similar to that for the Eastern European house mouse (M. musculus) and several other mammalian species. By contrast, among the many lab. strains that are known or suspected to stem from the pet mouse trade, there is little interstrain variation, most strains having the old inbred type of M. domesticus mtDNA, whose frequency in the wild mice examd. is low (.apprx.0.04). Also notable is the apparent homogeneity of mtDNA in M. domesticus races that have fixed .gtoreq.6 fused chromosomes and the close relationship of some of these mtDNAs to those of karyotypically normal mice. In addn., this paper discussed fossil and other evidence for the view that, in mice, as in may other mammals, the av. rate of point mutational divergence in mtDNA is 2-4% per million years. From this, it is estd. that the commensal assocn. between mice and human ancestors began >1,000,000 yr ago, i.e., at an early stage in the evolution of Homo erectus.

L8 ANSWER 94 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1982:541222 CAPLUS
DN 97:141222
TI Convenient procedures for SDS and conventional disc electrophoresis AU Neff, Jerry L.; Muniz, Nehemias; Colbourn, Joseph L.; De Castro, Aurora F. CS Res. Prod. Div., Miles Lab., Inc., Elkhart, IN, 46515, USA SO Electrophor. '81 [Eighty-One], Proc. Int. Conf., 3rd (1981), 49-63. Editor(s): Allen, Robert Chadbourne; Arnaud, Philippe. Publisher: de Gruyter, Berlin, Fed. Rep. Ger.

CODEN: 48KUAG
DT Conference
LA English
AB Proteins were sepd. by the title procedures by using performulated reagents included in the Canalco |SAGE| kit. Results are shown for human serum, spinal fluid, and saliva proteins; polynucleotide phosphorylase prepns. in different stages of purifn.; and for |RNA| polymerase subunits. Considerations and systemic error detn. for use of SDS polyacrylamide gel electrophoresis in mol. wt. detn. are described.

L8 ANSWER 95 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1979:116350 CAPLUS
DN 90:116350
TI Content of phosphorous compounds in Salvia seedlings grown in the light and in the dark, and treated with gibberellic acid
AU Khristov, Kh.
CS Metodi Popov Inst. Plant Physiol., Sofia, Bulg.
SO Fiziol. Rast. (Sofia) (1978), 4(3), 36-42
CODEN: FIRADV
DT Journal
LA Bulgarian
AB Culturing S. sclarea seedlings for 7 days on paper satd. with 0.0001% gibberellic acid (I) [77-06-5] at 1800 lx lighting caused less elongation than did culturing in the dark without I. I had not induced addnl. elongation in the dark-grown seedlings after 7 days, and only a slight elongation was noticeable after 3 and 5 days of culturing. I decreased the solid level in the light-grown seedlings by 22-6%, and decreased the proportion of org. P (P of |DNA| , |RNA| , phospholipids, phosphoproteins, and P compds. sol. in carboxylic acids) in the total P of the seedlings. I treatment raised the proportions of nucleic acids, phospholipids, and phosphoproteins in the light-grown seedlings. Dark culturing raised the level of P compds. sol. in carboxylic acids, and decreased the proportions of nucleic acids, phospholipids, and phosphoproteins in comparison with the light-grown seedlings which showed an increase in the proportion of nucleic acids, phospholipids, and phosphoproteins during the 7 days of culturing.

L8 ANSWER 96 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1971:51858 CAPLUS
DN 74:51858
TI Effect of 1-.beta.-D-arabinofuranosylcytosine on cell cycle passage time AU Karon, Myron; Shirakawa, Shigeru
CS Div. Hematol., Children's Hosp., Los Angeles, Calif., USA SO J. Nat. Cancer Inst. (1970), 45(5), 861-7
CODEN: JNCIAM
DT Journal
LA English
AB In fibroblast cultures 1-.beta.-D-arabinofuranosylcytosine (I) interfered most with the pas |sage| of cells from S to G2 phase. The magnitude of this effect was related to the dose and duration of I administration. Al-though 1 and 10 .mu.g I/ml produced the same decrease in cell labeling by tritiated thymidine, only the larger dose had significant effects on plating efficiency and cell transit rate, indicating that the inhibition of |DNA| synthesis is only 1 aspect of the mechanism of I action at the cellular level.

L8 ANSWER 97 OF 97 CAPLUS COPYRIGHT 2001 ACS
AN 1969:457688 CAPLUS
DN 71:57688
TI Heredity and chromatographic analysis of the anthocyanic pigmentation in the flowers and bracts of Salvia horminum
AU Cornu, A.; Paynot, Michel
CS Centre Rech. Agron., Dijon, Fr.
SO Ann. Amelior. Plant. (1969), 19(1), 5-13
CODEN: AAPLA8
DT Journal
LA French
AB The work material included 4 types: alba, the white flowers and bracts of which contain flavonoids but no anthocyanin; rosea, with pink flowers and bracts, with the prevailing pigment pelargonidin; Cardamine, with carmine-hued flowers and bracts contg. in its flowers as much cyanidin as pelargonidin; violacea, with purple flowers and bracts whose prevalent pigment is delphinidin in the flowers and petunidin in the bracts. All these pigments are 3-5 diglucosides acylated by p-coumaric acid. Three major |genes| appear to be accountable for the anthocyanin pigmentation of these flowers: |gene| A, prevalent and whose presence is necessary for synthesizing anthocyanin; |gene| R, which in the presence of A, accounts for the purple phenotype and for the synthesis it brings about in the bracts and flowers; |gene| C, highly active in the presence of Arr genotypes and accountable for the intensification of flower synthesis.

=> s ((serial (w) analysis) (5a) (gene (w) expression))/bi,ab
17184 SERIAL/BI
16406 SERIAL/AB
1028102 ANALYSIS/BI
18056 ANALYSIS/AB
588443 GENE/BI
401986 GENE/AB
470178 EXPRESSION/BI
403202 EXPRESSION/AB
L10 34 ((SERIAL (W) ANALYSIS) (5A) (GENE (W) EXPRESSION))/BI,AB
=> s (nonannotated (w) open (w) reading (w) frame#)/bi,ab

6 NONANNOTATED/BI
5 NONANNOTATED/AB
143827 OPEN/BI
136193 OPEN/AB

```
 40037 READING/BI
 38193 READING/AB
 68875 FRAME#/BI
 66050 FRAME#/AB
L11 1 (NONANNOTATED (W) OPEN (W) READING (W)
FRAME#)/BI,AB
=> s (non(w)annotated(w)open(w)reading(w)frame#)/bi,ab

 420583 NON/BI
 366280 NON/AB
 970 ANNOTATED/BI
 572 ANNOTATED/AB
 143827 OPEN/BI
 136193 OPEN/AB
 40037 READING/BI
 38193 READING/AB
 68875 FRAME#/BI
 66050 FRAME#/AB
L12 1
(NON(W)ANNOTATED(W)OPEN(W)READING(W)FRAME#)/BI,AB
=> s (nonannotated(w)orf#)/bi,ab

 6 NONANNOTATED/BI
 5 NONANNOTATED/AB
 10841 ORF#/BI
 9415 ORF#/AB
L13 0 (NONANNOTATED(W)ORF#)/BI,AB

=> s (non(w)annotated(w)orf#)/bi,ab

 420583 NON/BI
 366280 NON/AB
 970 ANNOTATED/BI
 572 ANNOTATED/AB
 10841 ORF#/BI
 9415 ORF#/AB
L14 0 (NON(W)ANNOTATED(W)ORF#)/BI,AB

=> d his


 (FILE 'HOME' ENTERED AT 10:41:47 ON 05 JAN 2001)

 FILE 'CAPLUS' ENTERED AT 10:41:53 ON 05 JAN 2001
L1 2854 S SAGE/BI,AB
L2 0 S NORF/BI/AB
L3 16 S NORF/BI,AB
L4 1050532 S (GENE# OR DNA# OR CDNA# OR RNA# OR
MRNA#)/BI,AB L5 2869 S L1 OR L3
L6 167 S L4 AND L5
L7 167 S L6 NOT 2001/PY
L8 97 S L7 NOT 2000/PY
L9 50 S L8 NOT 1999/PY
L10 34 S ((SERIAL (W) ANALYSIS) (5A) (GENE (W)
EXPRESSION))/BI,AB L11 1 S (NONANNOTATED (W) OPEN (W)
READING (W) FRAME#)/BI,AB L12 1 S
(NON(W)ANNOTATED(W)OPEN(W)READING(W)FRAME#)/BI,AB L13
0 S (NONANNOTATED(W)ORF#)/BI,AB
L14 0 S (NON(W)ANNOTATED(W)ORF#)/BI,AB

=> s l10 or l11 or l12 or l13 or l14

L15 36 L10 OR L11 OR L12 OR L13 OR L14

=> s l15 not 2001/py

 8521 2001/PY
L16 36 L15 NOT 2001/PY

=> s l15 not 2000/py

 852055 2000/PY
L17 23 L15 NOT 2000/PY

=> s l17 not l8

L18 1 L17 NOT L8

=> d l18 1 bib ab


L18 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2001 ACS
AN 1999:788799 CAPLUS
DN 132:118025
TI Large-scale analysis of the yeast genome by
transposon tagging and gene disruption
AU Ross-Macdonald, Petra; Coelho, Paulo S. R.; Roemer,
Terry; Agarwal, Seema; Kumar, Anuj; Jansen, Ronald;
Cheung, Kel-Hoi; Sheehan, Amy; Symoniatis, Dawn;
Umansky, Lara; Heldtman, Matthew; Nelson, F. Kenneth;
Iwasaki, Hiroshi; Hager, Karl; Gerstein, Mark; Miller,
Perry; Roeder, G. Shirleen; Snyder, Michael
CS Department of Molecular, Cellular and Developmental
Biology, Yale University, New Haven, CT, 06520-8103,
USA
SO Nature (London) (1999), 402(6760), 413-418
 CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB Economical methods by which gene function may be
analyzed on a genomic scale are relatively scarce. To
fill this need, we have developed a transposon-tagging
strategy for the genome-wide anal. of disruption
phenotypes, gene expression and protein localization,
and have applied this method to the large-scale anal.
of gene function in the budding yeast Saccharomyces
cerevisiae. Here we present the largest collection of
defined yeast mutants ever generated within a single
genetic background-a collection of over 11,000
strains, each carrying a transposon inserted within a
region of the genome expressed during vegetative
growth and/or sporulation. These insertions affect
nearly 2,000 annotated genes, representing about
one-third of the 6,200 predicted genes in the yeast
genome. We have used this collection to det.
disruption phenotypes for nearly 8,000 strains using
20 different growth conditions; the resulting data
sets were clustered to identify groups of functionally
related genes. We have also identified over 300
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previously |non| - |annotated| |open| |reading| |frames| and analyzed by indirect immunofluorescence over 1,300 transposon-tagged proteins. In total, our study encompasses over 260,000 data points, constituting the largest functional anal. of the yeast genome ever undertaken.
RE.CNT 30
RE
(2) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(3) Burns, N; Genes Dev 1994, V8, P1087 CAPLUS
(5) Christman, M; Cell 1988, V55, P413 CAPLUS
(6) Chu, S; Science 1998, V282, P699 CAPLUS
(7) DeRisi, J; Science 1997, V278, P680 CAPLUS
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